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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:07:00 ; Search time 14 Seconds

(Without alignments)
1347.981 Million cell updates/sec

Title: US-09-899-429a-2
Perfect score: 2487
Sequence: 1 MGISTVPEDLPLVLELV.....DIEALCGPALPAPSRLR 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2487	100.0	455	TR1A_HUMAN	P19438 homo sapien
2	1738	69.9	461	TR1A_PIG	P50555 sus scrofa
3	1563.5	62.9	461	TR1A_RAT	P22934 rattus norv
4	1521	61.2	454	TR1A_MOUSE	P25118 mus musculu
5	1517	61.0	471	TR1A_BOVIN	O19131 bos taurus
6	374	15.0	417	TR12_HUMAN	O33038 h tumor nec
7	251.5	10.1	435	TNR3_HUMAN	P36941 homo sapien
8	240.5	9.7	427	TR16_HUMAN	P08138 homo sapien
9	230	9.2	417	TR16_MOUSE	O22041 mus musculu
10	223	9.0	425	TR16_RAT	P07174 rattus norv
11	215	8.6	440	TR10B_HUMAN	O14763 homo sapien
12	212	8.5	381	TNR3_MOUSE	O9qzm4 mus musculu
13	207.5	8.3	415	TR23_MOUSE	P0284 mus musculu
14	205.5	8.3	176	TR23_MOUSE	O9erf3 mus musculu
15	205	8.2	474	TR1B_MOUSE	P25119 mus musculu
16	201.5	8.1	180	TR22_MOUSE	O9erf2 mus musculu
17	200	8.0	326	VT2_MYXL	P29835 myxoma viru
18	196.5	7.9	416	TR16_CHICK	P18519 gallus gall
19	193	7.8	468	T10A_HUMAN	O00220 homo sapien
20	192	7.7	325	VT2_SFVKA	P25943 Shope fibro
21	191	7.7	332	TNR6_PIG	O77736 sus scrofa
22	189.5	7.6	327	TNR6_MOUSE	P25446 mus musculu
23	183.5	7.4	461	TR1B_HUMAN	P20333 homo sapien
24	179	7.2	269	TNR5_BOVIN	O28203 bos taurus
25	177	7.1	335	TNR6_HUMAN	P25445 homo sapien
26	176.5	7.1	289	TNR5_MOUSE	P27512 mus musculu
27	175.5	7.1	323	TNR6_BOVIN	P21867 bos taurus
28	174	7.0	324	TNR6_RAT	O63199 rattus norv
29	169.5	6.8	655	TR21_MOUSE	O9epus mus musculu
30	169	6.8	351	CRMB_COMPX	O73559 compox viru
31	168	6.8	401	T11B_HUMAN	O00300 homo sapien
32	167	6.7	401	T11B_RAT	O08727 rattus norv
33	166.5	6.7	277	TNR5_HUMAN	P25942 homo sapien

ALIGNMENTS

RESULT 1	ID	TR1A_HUMAN	STANDARD:	PRT:	455 AA.
AC	P19438;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p50)				
DE	binding protein 1 (TBP1)				
GN	TNFRSF1A OR TNFR1 OR TNFR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=90235285; PubMed=2158863;				
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,				
RA	Geltanaga T., Granger G.A., Lentz R., Raab H., Kohn W.J., Goeddel D.V.;				
RT	"Molecular cloning and expression of a receptor for human tumor				
RT	necrosis factor.";				
RL	Cell 61:361-370(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90235284; PubMed=2158862;				
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,				
RA	Tabuchi H., Lesslauer W.;				
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis				
RT	factor receptor.";				
RL	Cell 61:351-359(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.				
RX	MEDLINE=91006021; PubMed=1698610;				
RA	Nopar Y., Kemper C., Brekebusch C., Engelmann H., Zhang R.,				
RA	Aderka D., Holtmann H., Wallach D.;				
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA				
RT	for the type I TNF-R, cloned using amino acid sequence data of its				
RT	soluble form, encodes both the cell surface and a soluble form of the				
RT	receptor.";				
RL	EMBO J. 9:3269-3278(1990).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91090841; PubMed=1702293;				
RA	Himmeler A., Maurer-Fogy I., Kroeck M., Scheurich P., Pfizenmaier K.,				
RA	Lantz M., Olsson I., Hauptmann R., Stretova C., Adolf G.R.;				
RT	"Molecular cloning and expression of human and rat tumor necrosis				
RT	factor receptor chain (p50) and its soluble derivative, tumor				
RT	necrosis factor-binding protein.";				
RL	DNA Cell Biol. 9:705-715(1990).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	TISSUE=Placenta;				
RC	MEDLINE=91017509; PubMed=2170974;				
RA	Gray P.W., Barrelet K., Chantry D., Turner M., Feldman M.;				

Query Match 100.0%; Score 2487; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-166;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSTVPDILLPLVLLLELVGIVPSGYIGLVPHLGDRKSDVCPQKQYTHPQNNISCTT 60
 DB 1 MGSTVPDILLPLVLLLELVGIVPSGYIGLVPHLGDRKSDVCPQKQYTHPQNNISCTT 60
 QY 61 KCHKGTLYVNDGPGDDTDCRECESSFTASENHLRHCLSCSKCRKEMQVEISSCTVD 120
 DB 61 KCHKGTLYVNDGPGDDTDCRECESSFTASENHLRHCLSCSKCRKEMQVEISSCTVD 120
 QY 121 RDTVCGCRKNQYRHYSENLFQCFNCSICLNGTVHLSQCEKQNTVCTCHAGFLRENECV 180
 DB 121 RDTVCGCRKNQYRHYSENLFQCFNCSICLNGTVHLSQCEKQNTVCTCHAGFLRENECV 180
 QY 181 SCGNCKKSELETKLCLPQIENYKGTEDSGTTLPLVYIFFGCLLSLFLGLMRYQRMK 240
 DB 181 SCGNCKKSELETKLCLPQIENYKGTEDSGTTLPLVYIFFGCLLSLFLGLMRYQRMK 240
 QY 241 SKLYSTVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 DB 241 SKLYSTVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 QY 301 PGDCPNFAAPRREYAPYQCADPLATATASDPIPNPLQKWEDESAHKPQSLDTPDPTLY 360
 DB 301 PGDCPNFAAPRREYAPYQCADPLATATASDPIPNPLQKWEDESAHKPQSLDTPDPTLY 360
 QY 361 AVEENVPPLWKEFEVRLGSDHEIDRLQNGRCLEADAYSMTATRRRTPREATLEL 420
 DB 361 AVEENVPPLWKEFEVRLGSDHEIDRLQNGRCLEADAYSMTATRRRTPREATLEL 420
 QY 421 LGRVLRMDLGLCLEDIEELALCGPAALPAPSLLR 455
 DB 421 LGRVLRMDLGLCLEDIEELALCGPAALPAPSLLR 455

RESULT 2
 ID TRIA_PIG STANDARD; PRT; 461 AA.
 AC P50555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 GN (TNF-R1) (TNF-R1) (p55).
 OS TNFRSF1A OR TNFR1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96011645; PubMed=7590278;
 RA Suter B., Paul U.H.;
 RT Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
 RT receptor.";
 RL Gene 163:263-266(1995).
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
 caspase-8 to the activated receptor. The resulting death-inducing
 signaling complex (DISC) performs caspase-8 proteolytic activation
 which initiates the subsequent cascade of caspases (aspartate-
 specific cysteine proteases) mediating apoptosis (By similarity).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 DR EMBL: U1994; AAC48499.1; -.
 DR HSSP: P19438; 1TNR.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF000020; TNFR_c6; 3.
 DR Pfam: PF00531; death; 1.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS0017; TNFR_NGFR_2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR Receptor: Apoptosis; 21
 FT SIGNAL 1 21
 FT CHAIN 22 461
 FT FT
 FT DOMAIN 22 210
 FT TRANSMEM 211 233
 FT DOMAIN 234 461
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 195
 FT DOMAIN 340 350
 FT DOMAIN 362 447
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 194
 FT DISULFID 185 190
 FT CARBOHYD 54 54
 FT CARBOHYD 86 86
 FT CARBOHYD 145 145
 FT CARBOHYD 151 151
 SQ SEQUENCE 461 AA: 50696 MW: CD72361EC60C9D43 CRC64;
 Query Match 69.9%; Score 1738; DB 1; Length 461;
 Best Local Similarity 71.6%; Pred. No. 2.3e-114;
 Matches 331; Conservative 29; Mismatches 94; Indels 8; Gaps 4;

QY 1 MGSTVPDILLPLVLLLELVGIVPSGYIGLVPHLGDRKSDVCPQKQYTHPQNNISCTT 60
 DB 1 MGSTVPDILLPLVLLLELVGIVPSGYIGLVPHLGDRKSDVCPQKQYTHPQNNISCTT 60
 QY 61 KCHKGTLYVNDGPGDDTDCRECESSFTASENHLRHCLSCSKCRKEMQVEISSCTVD 120
 DB 61 KCHKGTLYVNDGPGDDTDCRECESSFTASENHLRHCLSCSKCRKEMQVEISSCTVD 120
 QY 121 RDTVCGCRKNQYRHYSENLFQCFNCSICLNGTVHLSQCEKQNTVCTCHAGFLRENECV 180
 DB 121 RDTVCGCRKNQYRHYSENLFQCFNCSICLNGTVHLSQCEKQNTVCTCHAGFLRENECV 180
 QY 181 SCGNCKKSELETKLCLPQIENYKGTEDSGTTLPLVYIFFGCLLSLFLGLMRYQRMK 240
 DB 181 SCGNCKKSELETKLCLPQIENYKGTEDSGTTLPLVYIFFGCLLSLFLGLMRYQRMK 240

Db 181 SCVNCNA-DCKNLCPAISETRNDPDTGTVALPVIFGGLAFPLVGLACRQRMK 239
Qy 241 SKLVSVCKSPTEKKEGEGTTKP-LAPNPSFSPGPTPLGSPVSSFTSSSTY 299
Db 240 PKLYSLICKSKSPYKGEPEPLATAPSPITTFSPISPSPTTSSPVSFSPISPF 299
Qy 300 TEGDCENF--AAPRRVAPPYGADPILATAPASDPINPFLQKEDSAHK---PQSLDT 353
Db 300 TPCDMSNIVTSPPEKIAPPGACPIPLPMPASTVPPLPPLKWCSSAHSAPQALAD 359
Qy 354 DDPATLYAVENPPPLRMEFEVRRLGLSDHEIDRLONGRCIREQVSMATWRRRTER 413
Db 360 AAPATLYAVDGPPTPRMEFEVRRLGLSEHEIDRLONGRCIREQVSMATWRRRTSR 419
Qy 414 REATTELLGRVLDMDLGLCLEDIEBALGCPALPPAPSLLR 455
Db 420 REATTELLGSVLRDMDLGLCLEDIEBALGCPALPPAPSLLR 461
RESULT 3
TRIA_RAT STANDARD; PRT; 461 AA.
ID P22934: 091Y93: 091Y93:
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;
RA Himmler A., Maurer-Fogy I., Kiroenke M., Schurich P., Pfizenmaier K.,
RA Lantier M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RT necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.
RC STRAIN=Various;
RA Fureya T., Salstrom J.L., Bina J., Hashiramoto A., Dobbins D.E.,
RA Wilder R.L., Remmers E.F.;
RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus
RT among autoimmune susceptible and resistant inbred rat strains.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC EMBL: M63122; AAA4256.1; -
DR EMBL: AF329976; AAK53562.1; -
DR EMBL: AF329977; AAK53563.1; -
DR EMBL: AF329981; AAK53567.1; -
DR EMBL: AF329978; AAK53564.1; -
DR EMBL: AF329979; AAK53565.1; -
DR EMBL: AF329980; AAK53566.1; -
DR PIR: B3655; B3655.
DR HSP: P19438; INCR.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR Pfam: PF00531; death; 1.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 461
FT
FT DOMAIN 22 211
FT TRANSMEM 212 234
FT DOMAIN 235 461
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT DOMAIN 344 354
FT DOMAIN 363 448
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 195
FT DISULFID 185 191
FT CARBOHYD 54 54
FT CARBOHYD 151 151
FT CARBOHYD 201 201
FT VARIANT 230 230
FT VARIANT 295 295
SQ SEQUENCE 461 AA: 50969 MW: 52300 DA/BK, F344/NSHD, ACI/SGHSD,
Best Local Similarity 64.9%; Pred. No. 3.5e-102;
Matches 294; Conservative 46; Mismatches 104; Indels 9; Gaps 4;
Qy 1 MGLSTVPDLPLPVLELLVGYIPSGVIGLPHLDREKRDSPQGYIHPQNNISCT 60
Db 1 MGLPIVPGLLSLVALLLMGHPGVTGLPSLDGRKRLMLCPQGYAHPKNNISCT 60
Qy 61 KHKHGTLYLNDPFGQGLDCEKESGSGFTASENHLRGLSCSKRKKEGYEISCTVD 120
Db 61 KHKHGTLYLNDPFGQGLDCEKESGSGFTASENHLRGLSCSKRKKEGYEISCTVD 120
Qy 121 RPTVCGCRKNQVRHWSENLFQCFNCSICLNGTVHLSOCEKNTQCTGAGFLENQCV 180
Db 121 MDVVGCKKNQVRHWSENLFQCFNCSICLNGTVHLSOCEKNTQCTGAGFLENQCV 180

FT	VARSPLIC	54	98	MISSING (IN ISOFORM 6, ISOFORM 7 AND ISOFORM 9).
FT	VARSPLIC	54	236	MISSING (IN ISOFORM 8).
FT	VARSPLIC	156	171	SRRIDTCCTGLPEFE -> HPSVTLGGRPHSSTS (IN ISOFORM 7).
FT	VARSPLIC	172	417	MISSING (IN ISOFORM 7).
FT	VARSPLIC	182	417	MISSING (IN ISOFORM 5 AND ISOFORM 6).
FT	VARSPLIC	182	200	STLSCGPCRCAVCGMROMFWQVLNLLGVPLDGA -> LSVAGRGVCV (IN ISOFORM 11).
FT	VARSPLIC	182	218	STLSCGPCRCAVCGMROMFWQVLNLLGVPLDGA -> VLGGAPPCGPPPMAGNHDPILHPIPLASQAQGYCR (IN ISOFORM 3).
FT	VARSPLIC	219	417	MISSING (IN ISOFORM 3).
FT	VARSPLIC	182	277	STLSCGPCRCAVCGMROMFWQVLNLLGVPLDGA -> TYRCHWPKRPYLADDEAGMEALTPPATNLSPDSATHTLA PRDSEKICITQVLY -> PPSILAAGPMAQAVSLVSAG GRVGSLGAMRVGELGTGEGRRRGATGTPPAFVSLGPG APGWCPGPPPMAGNHDPILHPIPLASQAQGYCR (IN ISOFORM 12).
FT	VARSPLIC	278	417	MISSING (IN ISOFORM 12).
FT	VARSPLIC	200	253	MISSING (IN ISOFORM 12).
FT	VARSPLIC	200	253	MEFWQVLNLLGVPLDGA -> SSMCAGNARRTGMDRGEAGEEG MEALTPPATNLH -> SRMCAGNARRTGMDRGEAGEEG
Query Match		15.0%;	Score 374;	DB 1; Length 417;
Best local similarity		28.3%;	Pred. No. 3.6e-19;	
Matches 131;	Conservative	49;	Mismatches 183;	Indels 100; Gaps 22;
QY	15	LLELVAGTYPGSVIGLVNHLGDREKRSDVCCQGXIHPONNSSICTCKHNKSTYUINDCPG	74	
Db	15	LLVLVLGARAG-----GTRSR-----COCAGDFHKIKTGLFCRCGRGPAHYLKAPETE	63	
QY	75	PGQDTDCHECESGSGFTASENHIR-HCLSCSKCRKMEOVEISSTCVDRDYCGCKRKNOYR	133	
Db	64	PGNSTCLVCCPDPTFLAENHHNSECACQACDEASQVALENCASAVADTRCGCKPGWFV	123	
QY	134	HWSBNLFQC-----FNCSLCIN-GTVH-----LSQEKQNVTVCCHAEFLRENQCYSC-	182	
Db	124	EC---QVSQCVSSSFYTQPRLCDGCALRHHRILCSSRDPTCCGTLCPBEFYHGDCQCYSCP	180	
QY	183	----SNCKRSLECTRIKLROIENWKGTEDSGTYVLLPLVFIFGGLCILSLFIIGLMRYQR	238	
Db	181	TSTLGSCPE--RCAVNC-----GWRQMHWQYLAGLIVPLLDAATLTYYTRH	226	
QY	239	-WKSXLVSIYCGKSTPEKEGLEGTTRYK---LAPNSFSFPFGTPTVLGFSPVPSSTFT	294	
Db	227	CWPHK-----PLVTADEAGMEALTPTPATNLSPDS-----AHILLAPPDSEKXC	272	
QY	295	S-----SYRTYTGDD-----CPNFA-----APRRVARPYGADPILATALASDPIDPML	338	
Db	273	TVOLVGNSEWTGYPETOBALCPQYTWMSDQLPRSLRG-	318	
QY	339	QKWEDSAIKPOSJLTDDEPATLYAAVENVPRLMKFEVRLGSDHEIDRLTONGRCURE	398	
Db	319	---ESPAGSPAMIAOPG-QLYDMADVAFARRMKEFVRTLDLRRELVAEVEYIGR-FRD	373	
QY	399	AQYSMLATWRRRTPRREATLELLGRVLRDMDLCCLEDIEBAL	441	
Db	374	QQYEMLKRMFOGP---AGLGAVYAALERMGIDGVEDLRSL	413	
RESULT 7				
ID	TNR3_HUMAN	STANDARD:	PRT:	435 AA.
AC	P36941;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DE	Tumor necrosis factor receptor superfamily member 3 precursor			
DE	(lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related protein) (Tumor necrosis factor C receptor).			
GN	LTR OR TNFRSF3 OR TNFR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=93252381; PubMed=8486360;
 RT Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.,
 "Construction and evaluation of a cDNA library of human 12p
 transcribed sequences derived from a somatic cell hybrid."
 RL Genomics 16:214-218(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP FUNCTION.
 RA MEDLINE=94225209; PubMed=8171323;
 RA Crowe P.D., van Arsden T.L., Walter B.N., Ware C.F., Hession C.,
 Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
 RT "A lymphotoxin-beta-specific receptor."
 RL Science 264:707-710(1994).
 RN [4]
 RP CHARACTERIZATION.
 RA MEDLINE=99223511; PubMed=10207006;
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
 RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 death in HeLa cells."
 RL J. Biol. Chem. 274:11868-11873(1999).
 RN [5]
 RP FUNCTION.
 RA MEDLINE=20261554; PubMed=10799510;
 RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
 Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 LIGHT-mediated apoptosis of tumor cells."
 RL J. Biol. Chem. 275:14307-14315(2000).
 CC - FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 LTA and LTb, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
 and TRAF5. May play a role in the development of lymphoid organs.
 CC - SUBUNIT: Self-associates.
 CC - CELLULAR LOCATION: Type I membrane protein.
 CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L04270; AAA36757.1;
 CC EMBL: BC026262; AAH26262.1;
 CC HSSP: P25942; 1CDF.
 DR HSP: HSC6718; LTBR.
 DR Gene: HSC6718; LTBR.
 DR MIM: 600979;
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 435
 FT TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 3.
 FT DOMAIN 31 227
 FT TRANSMEM 228 248
 FT DOMAIN 249 435
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 168
 FT TNFR-CYS 3.

FT REPEAT 169 211 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 148 BY SIMILARITY.
 FT DISULFID 142 167 BY SIMILARITY.
 FT DISULFID 170 185 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 435 AA; 46709 MW; 62462656022656f CRC64;
 Query Match 10.1%; Score 251.5; DB 1; Length 435;
 Best Local Similarity 29.7%; Pred. No. 1,3e-10;
 Matches 106; Conservative 33; Mismatches 133; Indels 85; Gaps 22;
 Db 11 GLATVPDLLLPVLVLLVGVPSGVIGLVPHLDREK-RDSVCPQKRYHPNNNSICCT 60
 Qy 2 GLSTVPDLLLPVLVLLVGVPSGVIGLVPHLDREK-RDSVCPQKRYHPNNNSICCT 60
 Db 11 GLATVPDLLLPVLVLLVGVPSGVIGLVPHLDREK-RDSVCPQKRYHPNNNSICCT 60
 Qy 61 KCHGTYLYNDCPFGQDPTDCEGSGFTASENHLRLCLSCSKRMQGVETISCTVD 120
 Db 61 RCPGTYVASAK-SRIPIVTCATCAENSYENHWNLTICQLCRQDDPVMGLEIAPCTSK 119
 Qy 121 RDTVCGCRKNQRYHVSSENFQCFNCSL---CLNGTVHLSQGE---KONTVCT-CHAGPFL 174
 Db 120 RKTGCRQCPGMCANAWA---LECHTCELLSDCPPTTELEKDEYKGNHNCVPCAKGHE 175
 Qy 175 RENECVSCNCKSKLECKLCLPQIENVKGTEDSGTT-----VL 214
 Db 176 -QNTSSPBARCQPTHCNGL--VEAPGTAQSDTCKNPLPPEMSGTMMLAVLL 232
 Qy 215 PLVTFPGCLSLFLTGIMRYRWKS-----KLYSVCKSKTPKKGELGTTTKPLA 268
 Db 233 PLAEFL--LTAIVFSCF-----WKSHPSLCKRIGSL--KRRQCGG----- 270
 Qy 269 PNP---SFSPPG--FPTLGFSPV--SSTFSSTYVPGDQPNFAARRVAPPYO 319
 Db 271 PNPVAGSNEPKAPHPFDVLQPLPISGDVSPVSTGLP-----APVLEAGVPOO 321
 RESULT 8
 TR16_HUMAN STANDARD; PRT; 427 AA.
 ID TR16_HUMAN
 AC P08138;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
 affinity nerve growth factor receptor) (NGF receptor) (gp80-LNGFR)
 DE (p75 NTR) (Low affinity neurotrophin receptor p75NTR).
 GN NGFR OR TNFRSF16.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87051725; PubMed=3022937;
 RA Johnson D., Lianhan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
 Bothwell M., Chao M.;
 RT "Expression and structure of the human NGF receptor."
 RL Cell 47:545-554(1986).
 RN [2]
 RP SEQUENCE OF 1-22 FROM N.A.
 RA MEDLINE=89096903; PubMed=2850481;
 RA Sehgal A., Palli N., Chao M.;
 RT "A constitutive promoter directs expression of the nerve growth factor
 receptor gene."
 RL Mol. Cell. Biol. 8:3160-3167(1988).

```

CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC and NT-4. Can mediate cell survival as well as cell death of
CC neural cells.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC associated cell death executor.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: N- AND O-glycosylated.
CC -1- PTM: Phosphorylated on serine residues.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL: M14764; AAB59544.1; -
DR EMBL: M21621; AAB36363.1; -
DR PIR: A25218; G0H0N.
DR HSSP: P07174; INGR.
DR Genew: HGNC:7809; NGFR.
DR MIM: 162010; -
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR Pfam: PF00531; death; 1.
DR SMART: SM00005; Death; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR Receptor: Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW Repeat; Phosphorylation; Signal.
FT FT 1 28
FT CHAIN 1 28
FT 29 427
FT DOMAIN 29 250
FT TRANSMM 251 272
FT 273 427
FT DOMAIN 31 64
FT REPEAT 66 107
FT REPEAT 108 146
FT REPEAT 148 188
FT REPEAT 344 421
FT DOMAIN 197 248
FT DISULFD 32 43
FT DISULFD 44 57
FT DISULFD 47 64
FT DISULFD 67 83
FT DISULFD 86 99
FT DISULFD 109 122
FT DISULFD 125 138
FT DISULFD 128 146
FT DISULFD 149 164
FT DISULFD 167 180
FT DISULFD 170 188
FT CARBOHYD 60
FT SEQUENCE 427 AA; 45183 MW; B09FA143B3D625B CMC64;
Query Match 9.7%; Score 240.5; DB 1; Length 427;
Best Local Similarity 23.8%; Pred. No. 7.7e-10;
Matches 116; Conservative 54; Mismatches 180; Indels 137; Gaps 25;
OY 12 PVLLELLVGLVPSGVILVPHLDGRKRDVCGPOGKIIPHOONSICCTCKHKGTLYLND 71
DB 13 PRLILLGLVSLGA-----KEACPGILYTH---SECECKACNLGEGVAP 56
OY 72 CPFGQPDHDCREC-ESGSGFTASENHLRHCLSCSKCRKEMGQVEISS-CTVDRDTPVCGGRK 129

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DB 57 C-GANO-TVCEPCLDSVTFSDVVSATPECKPCTEC---VGLQSMSPACEADAVRC-- 109
OY 130 NOYRHYWSENLFQCFNCISLINTG-VHLSQOEKONTVC-TCHAGFLRE-----NECVCS 183
DB 110 -AVGYQDETGTGCEACRCVCEAGSLVFCQDKQNTVCECPGRTYSDANHHVDPCLPT 168
OY 184 NC---KKSLECKKLCLEPOIENYKGTEDSGTVLLPLVIFGICLLSLFTGLMYRYQRN 239
DB 169 VEDETREQLRECTRMADACEETIPG-----RM 195
OY 240 KSLVSYIVGKSTPEKEGEGLETTKPLAPNPS---FSPPTGPTPLGSPVPSSFTFS 296
DB 196 -----ITRSTPEESDSTABSTOPEAPPEODLIATVAGVTTVMSSQPVVTRGTT 248
OY 297 STYTPGDCENFA-----PRREVAPPYGAD--PIATATLADPIPNPKQME 342
DB 249 DNLIPIYCSILAAVYVGLVAYIAFKRWNSCKQKQGANRPVQNT-----PPEGKLLS 303
OY 343 DS--AHKPSLDTPDPAFLYA-----VVENVPPLR-----WKEFV 375
DB 304 DSGISVDSQSLHDQOPHTOTASQALKGDGLYSILPAKREVERKTLNGSAGDTRHHA 363
OY 376 RRLGSDHEDLELQNGCLREAOYSMLATWRRTPRREATLELLGRVLRMDLLGCE 435
DB 364 GELGTOPEHID--SFTHEACPVR--LIASW---ATQDSATLALLAALRIQ---RA 411
OY 436 DIEALC 442
DB 412 DLVESLC 418

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RESULT 9
TR16_MOUSE STANDARD; PRT; 417 AA.
ID TR16_MOUSE
AC 0920M1:

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DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE affinity nerve growth factor receptor) (NGF receptor) (Low affinity
DE neurotrophin receptor p75NTR).
GN NGFR OR TNFRSF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A;
RX MEDLINE=99077793; PubMed=9857182;
RA Tuffreau C., Benejean J., Blondel D., Kieffer B., Flaman A.;
RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
RT receptor for rabies virus.";
RL EMO J. 17:7250-7259(1998).
CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC AND NT-4. Can mediate cell survival as well as cell death of
CC neural cells (By similarity). Binds to rabies virus glycoprotein
CC Gs.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC associated cell death executor (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- PTM: N- AND O-glycosylated (By similarity).
CC -1- PTM: Phosphorylated on serine residues (By similarity).
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL; AF105292; AAD17943.1; .
DR HSBP; P07174; INGR.
DR MGI; MGI:97323; Ngr.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR.1; 3.
DR PROSITE; PS50050; TNFR_NGFR.2; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW Repeat; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 1 417 TUMOR NECROSIS FACTOR RECEPTOR
FT 22 417 SUPERFAMILY MEMBER 16.
FT DOMAIN 22 246 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 247 265 POTENTIAL.
FT DOMAIN 266 417 CYTOPLASMIC (POTENTIAL).
FT REPEAT 24 57 TNFR-CYS 1.
FT REPEAT 59 100 TNFR-CYS 2.
FT REPEAT 101 139 TNFR-CYS 3.
FT REPEAT 141 181 TNFR-CYS 4.
FT REPEAT 181 411 DEATH.
FT DOMAIN 190 241 SER/THR-RICH.
FT DISULFID 25 36 BY SIMILARITY.
FT DISULFID 37 50 BY SIMILARITY.
FT DISULFID 40 57 BY SIMILARITY.
FT DISULFID 60 76 BY SIMILARITY.
FT DISULFID 79 92 BY SIMILARITY.
FT DISULFID 82 100 BY SIMILARITY.
FT DISULFID 102 115 BY SIMILARITY.
FT DISULFID 118 131 BY SIMILARITY.
FT DISULFID 121 139 BY SIMILARITY.
FT DISULFID 142 157 BY SIMILARITY.
FT DISULFID 160 173 BY SIMILARITY.
FT DISULFID 163 181 BY SIMILARITY.
FT CARBOHYD 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510DBA9F82 CRC64;

Query Match 9.28; Score 230; DB 1; Length 417;
Best Local Similarity 24.08; Pred. No. 4e-09;
Matches 120; Conservative 61; Mismatches 161; Indels 158; Gaps 30;

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QY 363 VENVPLMKFEVRLGSLDHEIDRLQLONGRCLEAGYSMLATWRRRTPREATLELG 422
DQ 349 -----WRHLAGELGQPEHID--SETHACPVRA---LLASGAD-----SATDLALL 392
QY 423 RVLKMDMLGCLDEIEALC 442
DQ 393 AALRIQ----RADIVESLC 408

RESULT 10
TR16_RAT STANDARD; PRT; 425 AA.
ID TR16_RAT
AC P07174;
DT 01-APR-1988 (Rel. 07, Created)
DT 15-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE "Tumor necrosis factor receptor superfamily member 16 precursor (low-
DE affinity nerve growth factor receptor) (NGF receptor) (p80-LNGFR)
DE (p75 ICD) (low affinity neurotrophin receptor p75NTR).
GN NGFR OR TNFRSF16.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-67115859; PubMed-3027580;
RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
RT "Gene transfer and molecular cloning of the rat nerve growth factor
RT receptor.";
RL Nature 325:593-597(1987).
RN [2]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver.
RX MEDLINE-93077038; PubMed-1446821;
RA Metcalf M., Timmusk T., Allikmets R., Saarma M., Persson H.;
RT "Regulatory elements and transcriptional regulation by testosterone
RT and retinoic acid of the rat nerve growth factor receptor promoter.";
RL Gene 121:247-254(1992).
RN [3]
RP STRUCTURE BY NMR OF 334-418.
RX MEDLINE-97449145; PubMed-9305641;
RA Ljepush E., Ilag L.L., Oetting G., Ibanez C.F.;
RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
RL EMDO J. 16:499-5005(1997).
CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC and NT-4. Can mediate cell survival as well as cell death of
CC neural cells.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC associated cell death executor.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: N- AND O-glycosylated.
CC -1- PTM: Phosphorylated on serine residues.
CC -1- SIMILARITY: CONTAINS 1 DEATH CYTS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL; X05137; CA28783.1; .
DR EMBL; X61269; -; NOT_ANNOTATED_CDS.
DR PIR; A26431; A26431.
DR PDB; INGR; 29-JUL-97.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR Pfam; PF00531; death; 1.

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DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
KW Repeat; Phosphorylation; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 425
FT DOMAIN 30 251
FT TRAMEM 252 273
FT REPEAT 274 425
FT REPEAT 32 65
FT REPEAT 67 108
FT REPEAT 109 147
FT REPEAT 149 189
FT DOMAIN 354 419
FT DISULFID 198 249
FT DISULFID 33 44
FT DISULFID 45 58
FT DISULFID 48 65
FT DISULFID 68 84
FT DISULFID 87 100
FT DISULFID 90 108
FT DISULFID 110 123
FT DISULFID 126 139
FT DISULFID 129 147
FT DISULFID 150 165
FT DISULFID 168 181
FT DISULFID 171 189
FT CARBOHD 61 71
FT CARBOHD 71 71
SQ SEQUENCE 425 AA; 45432 MW; B2E152D94D3827F8 CRC64;
Query Match 9.0%; Score 223; DB 1; Length 425;
Best Local Similarity 23.2%; Pred. No. 1,3e-08;
Matches 115; Conservative 50; Mismatches 170; Indels 160; Gaps 27;
OY 14 VLELLVIGYPSGVIGLVPHLDREKRDSPQGYIHPONNISICCTKCHKGTLYLNDGP 73
DB 16 LLLLLILGVSSGGA-----KETCSTGLYTH--SGECKACNLGEGVAQPC- 58
OY 74 GPGQDTRREC-ESGSFTASENHLRLCLSCSKCKEMQVEISS-CYUDROTVCCGRKQ 131
DB 59 GANQ-TVEPCIDNVTESDVVSATPECKPCTEC---LGQSKSAPCVADDAVNCRC--A 111
OY 132 YRHVSENLFOCFNCSLCLNGT-VHLSCQEKONTVC-TCHAGFPLRE---NECVSCSNC 185
DB 112 YGYODEFGHGCAGSCVCGSLVFCODKONTVCCECPREBTGDEANHVDPCLPCTVC 171
OY 186 ---KSLSECTKLCLEPQIENYAKGTDSGTYVLLPVIFPGCLLSLFTGLMYRQRMKS 241
DB 172 EDTREQLRECPFWADAECEELPG-----RW-- 196
OY 242 KLYSLVCGSKPEKGELEG-TTKPLAPNPSFPTPGTPTLGFSPVSSFTSSSTYT 300
DB 197 -----IRSTTP-----EGSDSTAPSTQDEPVPEQDLVSTVADMTVYGSSQPVYT 245
OY 301 PGDCNPAAPRRVAPRY-----QGAD-PILATATLAS 331
DB 246 RGTTON-----LIPVCSILAAYVGVIVIAFRNNSCQKONOGANSRNVNT----- 294
OY 332 DPTNPLOKWEDESAHKPOSLOTDPAI-----LVAV-----ENVPL- 369
DB 295 -PPPEGEKLHSDSGISVSQSLHDQOHTQTQVASQALKGDNLYSLPLTKREEVEKLLN 353
OY 370 --RWKEFVRRLGSLDHEIDRLONGRCRLREKQYSMLATWKRRTRRRATLELLRLVLD 427
DB 354 GDTWHLNLAGELGYOPEHD--STHEACPVR--LLASWGAQD--SATLDALLAALRR 405
OY 428 MDLLGLELIEDIERALC 442
DB 428 MDLLGLELIEDIERALC 442

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DB 406 IQ----RADIVESLC 416
RESULT 11
ID 110B_HUMAN STANDARD; PRT; 440 AA.
AC 014763; 015531; 015508; 015517; 014720; 09BVE0;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death
DE receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL
DE receptor-2) (TRAIL-R2).
GN TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND SEQUENCE OF N-TERMINUS.
RC TISSUE=foreskin fibroblast;
RX MEDLINE=97459925; PubMed=9311998;
RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,
RA Bolani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,
RA Goodwin R.C., Rauch C.T.,
RA "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";
EMBO J. 16:5386-5397(1997).
[2]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE
RP SPLICING.
RX MEDLINE=97431692; PubMed=9285725;
RA Scretion G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E.,
RA McMichael A.J., Bell J.I.;
RA "TRICK2, a new alternatively spliced receptor that transduces the
RT cytotoxic signal from TRAIL.";
RL Curr. Biol. 7:693-696(1997).
[3]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.
RC TISSUE=Liver, and Spleen;
RX MEDLINE=98039016; PubMed=9373179;
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,
RA Tschopp J.;
RL "Characterization of two receptors for TRAIL.";
PEBS Lett. 416:329-334(1997).
[4]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RC TISSUE-Ovary;
RX MEDLINE=97467719; PubMed=9326928;
RA Wu G.S., Burns T.F., McDonald E.R., III, Jiang W., Meng R.,
RA Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,
RA Splinter N.B., Markowitz S., Wu G., el-Deiry W.S.;
RT "Killer/DR5 is a DNA damage-inducible p53-regulated death receptor
RT gene.";
RL Nat. Genet. 17:141-143(1997).
[5]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE=97390508; PubMed=9242610;
RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;
RT "An antagonist decoy receptor and a death domain-containing receptor
RT for TRAIL.";
RL Science 277:815-818(1997).
[6]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE=97467318; PubMed=9325248;
RA MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T.,
RA Cohen G.M., Alnemri E.S.;
RT "Identification and molecular cloning of two novel receptors for the
RT cytotoxic ligand TRAIL.";
RL J. Biol. Chem. 272:25417-25420(1997).
[7]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE=98090092; PubMed=9430227;
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;

```

RT "Death receptor 5, a new member of the TNFR family, and DR4 induce
 RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";
 RL Immunol 7:821-830(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RX MEDLINE-97390509; PubMed-9242611;
 RA Sheridan J.P., Walters S.A., Pitti R.M., Gurney A., Stutch M.,
 RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,
 RA Goddard A.D., Godowski P., Ashkenazi A.;
 RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy
 RT receptors.";
 RL Science 277:818-821(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RA Aral T., Akiyama Y., Okabe S., Salto K., Iwai T., Yuasa Y.;
 RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2
 RT gene in colorectal carcinoma.";
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RA Cao X., Zhang W., Wan T.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RA Parra T., Vu T., Gilbert T., Gross J., O'Hara P.;
 RT "Home sapiens homolog of tumor necrosis factor receptor.";
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RC Tissue-Cervix;
 RA Strausberg R.;
 RL Submitted (Dec-2000) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.
 RX MEDLINE-20017054; PubMed-10549288;
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 RT complex with death receptor 5.";
 RL Mol. Cell 4:563-571(1999).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.
 RX PubMed-10542098;
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Screaton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RT specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
 CC adaptor molecule FADD recruits caspase-8 to the activated
 CC receptor. The resulting death-inducing signaling complex (DISC)
 CC performs caspase-8 proteolytic activation which initiates the
 CC subsequent cascade of caspases (aspartate-specific cysteine
 CC proteases) mediating apoptosis. Promotes the activation of NF-
 CC kappaB.
 CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/TRICK2B (SHOWN HERE)
 CC AND A SHORT FORM/TRICK2A. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;
 CC very highly expressed in tumor cell lines such as Hela S3, K562,
 CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral
 CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,
 CC ovary, uterine tract; not detectable in brain.
 CC -1- INDUCTION: TNFSF10 is regulated by the tumor suppressor p53.
 CC -1- DISEASE: Defects in TNFSF10B may be a cause of squamous cell
 CC carcinoma of the head and neck.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC or send an email to license@ebi.ac.uk).

CC EMBL; AF016849; AAC51778.1; -
 DR EMBL; AF016857; AAB70577.1; -
 DR EMBL; AF016858; AAB70578.1; -
 DR EMBL; AF016866; AAB81180.1; -
 DR EMBL; AF022386; AAB71949.1; -
 DR EMBL; AF012628; AAB67109.1; -
 DR EMBL; AF020501; AAB71412.1; -
 DR EMBL; AF016268; AAC01565.1; -
 DR EMBL; AF012535; AAB67103.1; -
 DR EMBL; AB014718; BAA33723.1; -
 DR EMBL; AB014710; BAA33723.1; -
 DR EMBL; AB014711; BAA33723.1; JOINED.
 DR EMBL; AB014712; BAA33723.1; JOINED.
 DR EMBL; AB014713; BAA33723.1; JOINED.
 DR EMBL; AB014714; BAA33723.1; JOINED.
 DR EMBL; AB014715; BAA33723.1; JOINED.
 DR EMBL; AB014716; BAA33723.1; JOINED.
 DR EMBL; AB014717; BAA33723.1; JOINED.
 DR EMBL; AF153687; AAF75587.1; -
 DR EMBL; AF192548; AAF07175.1; -
 DR EMBL; BC001281; AAF01281.1; -
 DR Genew; HGNC:11905; TNFSF10B.
 DR MIM; 603612; -
 DR MIM; 601400; -
 DR PDB; 1D0G; 22-OCT-99.
 DR PDB; 1D4V; 01-NOV-99.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF000020; TNFR_c6; 2.
 DR Pfam; PF00531; death; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
 DR PROSITE; PSS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PSS00500; TNFR_NGFR_2; 2.
 KW Receptor; Apoptosis; Transmembrane; Repeat; Signal;
 KW Alternative splicing; 3d-structure.
 FT SIGNAL 1 55
 FT CHAIN 1 56 440
 FT DOMAIN 56 210 TUMOR NECROSIS FACTOR RECEPTOR
 FT TRANSMEM 211 231 SUPERFAMILY MEMBER 10B.
 FT DOMAIN 232 440 EXTRACELLULAR (POTENTIAL).
 FT REPEAT 57 94 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 97 137 TNFR-CYS 1.
 FT REPEAT 138 178 TNFR-CYS 2.
 FT REPEAT 192 206 TNFR-CYS 3.
 FT REPEAT 207 223 TAPE.
 FT DOMAIN 339 422 DEATH.
 FT DOMAIN 423 440 POLY-GLY.
 FT DISULFID 81 94
 FT DISULFID 97 113
 FT DISULFID 116 129
 FT DISULFID 137 137

Query Match 8.68; Score 215; DB 1; Length 440;
 Best Local Similarity 23.08; Pred. No. 4.8e-08;
 Matches 109; Conservative 62; Mismatches 172; Indels 130; Gaps 22;

QY 6 VPDLPLVLELVLELVGVIPSGVI---GLVP--HLGDRKRS---VCPGKRYIHPOUNS 56
 DB 34 VPKLVLVVAVLVLLVLSKSLITQODLAPQQRAPQQRKSSPSGICPPHHHSDEGR 92
 QY 57 ICCTCKHKGTVLYNDCEPGQDTCRECSEG-SFTASENHLRHCLSCSKCKRKGQVEYS 115
 DB 93 -----DCISCKYGQDYSTHMDLDFCLACTRC--DSGEVELS 127
 QY 116 SCTVDRLTVCCCKRNQRYHWSNLLPQCFNCSL-CLNCTV-----HLSCKQKQNTV 165

Db	128	PCTTATNTVYCCCEETFEEDSPEN--CRKCTGCPRGKVKVGDCTPMSDICEYHKESSG-	184
Qy	166	CTCHAGFLRRENECSCSNCKKSLCTKLCLPQIENVNCTEDSGTTLVLPYIFFGCLL	225
Db	185	-TKSHGEAPVAEEVYTSSTPGTPASC-----SLSGITIGVVAAYLVIAVAVFC-K	233
Qy	226	SLLEFGLMYRYVRWMSKLYSI--VC--GKSPKEGELEGTTKFLAPNPSFSP-----T	276
Db	234	SLL-----MKKVLPLYLKIGICSGGGPDER--VDRSSQRGCAEDNVNLNELYSLIQ	280
Qy	277	PGFTPLTGFSSVPSSTFTSSSTTGTGDCPNFAP-----REYAPPYGCADPILATA	328
Db	281	PTVPEQMEQVEPEPEPPGVNMLSPGESEHLLPEAEARSORRLIYPANEG-----	332
Qy	329	LASPIPIPLKWEIDSAKPKQSLDDPATLYAAVENNPPLKWEFEVRLGSDHEIDL	388
Db	333	---DPTETLRQCFDFA-----DLYPDSMEPLMKRLGIMDEIT-KV	370
Qy	389	ELONGRCLEAQAQSMLATWRRTPTREATLELGHVLRDMDLGLEDIEEAL	441
Db	371	AKAEAGHRTDLYTLWLTKVKNKT-----GDAVHTLLDALETGLGERL	413

RESULT 12

ID	T10B_MOUSE	STANDARD;	PRT;	381 AA.
AC	Q9JUL6; Q9JUL5; Q9JUL6;			
DT	15-JUN-2002 (Ref. 41, Created)			
DT	15-JUN-2002 (Ref. 41, Last sequence update)			
DT	15-JUN-2002 (Ref. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (Mk).			
GN	TNFRSF10B OR DR5 OR KILLER.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	NCBI_TaxID=10090;			
	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=99310501; PubMed=10383128;			
RA	Mu G.S., Burns T.F., Zhan Y., Ahlemli E.S., El-Deiry W.S.;			
RT	"Molecular cloning and functional analysis of the mouse homologue of the killer/DR5 tumor necrosis factor-related apoptosis-inducing ligand (TRAIL) death receptor.";			
RL	Cancer Res. 59:2770-2775(1999).			
	[2]			
	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RA	Nakamura Y., Tamari M., Matanabe O.;			
RL	"Mouse TRAIL receptor.";			
RT	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-kappaB.			
CC	-1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.			
CC	-1- INDUCTION: TNFSF10B is regulated by the tumor suppressor p53.			
CC	-1- SIMILARITY: CONTAINS 3 TNF-CYS REPEATS.			
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
CC	-----			
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[illegible]

OY 406 TWRRTPREATTELLGRLVLDMDLGLCEIDEE 439
 DB 322 KWRHOT-----GRSASINHLDLALAEVER 345

RESULT 13
 TNR3_MOUSE STANDARD; PRT: 415 AA.

AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (Lymphotoxin-beta receptor).
 GN LTRR OR TNFRSF3 OR TNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxId=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression".
 RL J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping".
 RL Genomics 30:312-319(1995).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF6. May play a role in the development of lymphoid organs
 CC (By similarity).
 CC -1- SUBUNIT: Self-associates (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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DR EMBL: U29173; AAA68964.1; -;
 DR EMBL: L38423; AB00846.1; -;
 DR EMBL: U30798; AA81334.1; -;
 DR HSSP: O14763; ID0G.
 DR MGD: MGI:104875; Ltbr.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR ProDom: PD000771; TNFR_C6; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415
 FT TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPRAFAMILY MEMBER 3.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 224 244
 FT DOMAIN 245 415
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 81
 FT TNFR-CYS 1.
 FT REPEAT 82 124
 FT TNFR-CYS 2.
 FT REPEAT 125 170
 FT TNFR-CYS 3.

FT REPEAT 171 213 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 142 169 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 40 BY SIMILARITY.
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 415 AA; 44956 MW; 29B326A56AEF661 CRC64;

Query Match 8.3%; Score 207.5; DB 1; Length 415;
 Best local similarity 26.8%; Pred. No. 1.5e-07;
 Matches 96; Conservative 37; Mismatches 158; Indels 67; Gaps 17;

OY 2 GLSTVPDLLPLVLELLVGPVIGLVPHLGRDRSDVCPGKYIHPONNISCTK 61
 DB 11 GLAMP---LILGLSLGLVASQPQ---LVPPY--RIENQTCMDQDKRYEPMHDVCCSR 61

OY 62 CHKGTYLNDPGRPGQDTCRECESGSTASENHRHLSCKRKEGVEISSCTYDR 121
 DB 62 CPGEFVFAVC--SRQDVTCTCPHNSYNEHMHLSQCLRPDCIVIGFEVAPCTSDR 120

OY 122 DTVCGCRKQRYRWYSEMLFOCFNCS-----LCUNGTHLSQOEKONT---VCTCHAGPF 173
 DB 121 KAECRCQPGMAGCYILDN---ECVHCSEERLVLCQGTAEVTDIMTDVNCVPCPKGHF 177

OY 174 LRENECVSCSNCKSLSECTKLCLPOIENVKGTEDSGT-----TVLLPLVIF 219
 DB 178 --QNTSPRARCQPHTRCEIOGL--VEAPGYSVSDTICKNPPERGAMLLAILLSLVLF 233

OY 220 FGLCLSLFLFTGLM---YRQRMKSKLYSYVCKSGSTPEKEGELGTTTKPLAPPSRP 275
 DB 234 -----LLFTVYLACAMRHPSLCKRLGTL--KRHEGE-----ESPCCPAPRADP 277

OY 276 TPGFPTLGFSPVPSFTSSSTVTPGDCPPNAPRARVAPPGADPILATLASDP 333
 DB 278 ---HPDLAEPILPMSGLSPS---PAGPP--TAFSEEVYVLOQDSPVQARELENER 327

RESULT 14
 TR23_MOUSE STANDARD; PRT: 176 AA.

AC Q9ER63; ORVHC0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis
 DE factor receptor p60 homolog 1) (TNF receptor family member SOB).
 GN TNFRSF23 OR TNFRSFALI OR TNFRH1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxId=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV; TISSUE=Embryonic stem cells;
 RX MEDLINE=20519229; PubMed=11063728;
 RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
 RA Lane N., Reik W., Walter J.;
 RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
 RT implications for a novel imprinting centre and extended imprinting.";
 RT Hum. Mol. Genet. 9:2691-2706(2000).
 RL Hum. Mol. Genet. 9:2691-2706(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP Pan G., Mao W., Risse P.;
 RA "Characterization of SOB, a member of the TNFR family.";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -----

FT	CARBOHYD	69	69	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SO	SEQUENCE	474 AA;	50319 MM;	462EAE398C4D6563	CRC64;

Query Match	8.2%	Score 205	DB 1	Length 474
Best Local Similarity	26.4%	Pred. No.	2.6e-07	
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				Gaps 11

SO SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match	8.28;	Score 205;	DB 1;	Length 474;
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Best Local Similarity 26.4%; Pred. No. 2.6e-07;
Matches 67; Conservative 30; Mismatches 105; Indels 52; Gaps 11.

Matches 67; Conservative 30; Mismatches 105; Indels 52; Gaps 11;

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QY      44  CPGCKYTHPPNNNSICCKCHNGTYLYNDCCGGDDTCRECEGSGFTASNNHLRHCLSC- 102
Db      40  CQISEGYEYDRKAQMCCKACPPGGVYVHKFC- NKISDTYCACCEASMTQVANNQRTCLSCS 98

QY      103  SKCKREKGOVEISCTYVDRODTVCCGRKNQY----RHYNSNLFQCFNCISJCLNG- TVHUS 157
Db      99  SSCSTTD--QVEIRCTCKOONRVCAECBGRYCALKTH--SSGSCROCMRLSCGCGGFGVASS 154

QY      158  CQEKONTVVC--CHAGFFLRENECVSCSNCKSLSECTKLCIJOEYENVG--TEBGGTVLL 214
Db      155  RAPGNVLTCKKCACTGF--SITTSSTDYCRPHRCLSTLAIPGAASNDVAVCAPESPILSAI 212

QY      215  PLVTFEGICLLSLFLIGLIMRYRQWMSKSLYSIVCGSKTPEKEGELEGTTRKPLAPNFSF 274
Db      213  PRLTYLV-----SQPEP-----TRSQPIDQEGPFS 236

QY      275  PTPGFTPIHLSFV 288
Db      237  QTPSILTVSLGSTPI 250

```

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Db      | : : | | | : : | | | : | | | |
40 CQISQEYDRAKQMCACAKSPGQYVKHFC-NKTSDTVACADCEASMYQTQVWNQFRTCLCS 98

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0y      103 SKCKREMGVEISSCVDRDVYCGCRKNQY-----RHYSNENLPQFNCSLCLNG-IVHLS 157
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      99 SSGFTD--QVEIRACTKQGNRYCACEAGRYCAIKTH--SGSCRCQMRLSKCGPGFGVASS 154

```

Db 99 SSCTD--QVEIRACTKQONRVACACEAGRYCALKTH--SGSCRQCMRLSKCGPGFGVASS 154

158 CQEKONTVC-TCHAGFLRENECVSCSNCKKSELECTKICLPQIENVKG--TEDSGTVLL 214

Db 155 RAPNGNVLCKACAPGTF--SDTTSTSDVCRPHRICSLAIPGNASTDAVCAPEPTLSAI 212

QY 215 PLVIFGCLLSLFIGLMYRQRWKSKLYSIVCGKSTPEKEGELEGTTPKPLAPNPSFS 274

Db 213 PRTLY-----SQPE-----TRSQPLDQEPGPS 236

Qy 275 PTPGFTPTLGFSpv 288

Db 237 QTPSILTSLGSTPI 250

Search completed: December 27, 2002, 15:08:38
Job time : 15 secs

Job time : 15 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:06:59 ; Search time 40 Seconds

(without alignments)
1515.726 Million cell updates/sec

Title: US-09-899-429a-2

Perfect score: 2487
Sequence: 1 MGLSTVPDLPLPLVLELV.....DIEALCPALPPAPSLR 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
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5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
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22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2487	100.0	455	12 AAR10986	30kd TNF inhibitor
2	2487	100.0	455	14 AAR42059	Lambda derived TNF
3	2487	100.0	455	16 AAR75084	p55 TNF-R, Homo s
4	2487	100.0	455	20 AAY30934	Human tumour necro
5	2487	100.0	455	21 AAB35266	Human tumour necro
6	2487	100.0	455	21 AAB37800	Human tumour necro
7	2487	100.0	455	21 AAB26984	Human TNFR 1, Hom
8	2487	100.0	455	21 AAB23446	Human tumour necro
9	2487	100.0	455	21 AAB01336	TNF-R1 death recep
10	2487	100.0	455	22 AAB86817	Human TNFRP-associ

11	2487	100.0	455	22 AAB36697	Human tumour necro
12	2487	100.0	455	22 AAB37677	Human 30 kDa TNF 1
13	2487	100.0	455	23 AAB81649	Human tumour necro
14	2487	100.0	455	23 AAU75064	Human tumour necro
15	2484	99.9	455	12 AAR11082	Human 55kd TNF-D1n
16	2481	99.8	455	13 AAR20787	TNF-alpha binding
17	2478	99.6	455	14 AAR42197	p55 Tumour necrosi
18	2475	99.5	455	14 AAR51034	Mutant p55 tumour
19	2471	99.4	455	11 AAR07451	Human Tumour Necro
20	2464	99.1	455	12 AAR12550	Type I TNF recepto
21	2463.5	99.1	909	19 AAB64485	Human Fas protein.
22	2462	99.0	455	13 AAR24000	TNF-alpha 55kd rec
23	2457	98.8	453	22 AAB50895	Human TNFR 1, Hom
24	2417	97.2	443	14 AAR51033	Mutant p55 tumour
25	2365	95.1	433	14 AAR51032	Tumour Necrosis fa
26	2053	82.5	371	11 AAR07449	Tumour Necrosis fa
27	1558	62.6	280	22 AAB66979	Tnfr1 protein.
28	1539.5	61.9	461	11 AAR07450	Ret Tumour Necrosi
29	1192	47.9	211	20 AAB89225	Tumour necrosis fa
30	1192	47.9	311	20 AAB89229	Tumour necrosis fa
31	1192	47.9	366	20 AAB89228	Tumour necrosis fa
32	1192	47.9	397	20 AAB89227	Tumour necrosis fa
33	1192	47.9	417	20 AAB89226	Tumour necrosis fa
34	1192	47.9	420	20 AAB89224	Tumour necrosis fa
35	1130	45.4	199	13 AAR24080	Truncated TNF-alpha
36	1093.5	44.0	547	16 AAR70104	TNF-R-GBP fusion
37	1093	43.9	309	16 AAR70108	TNF-R-GBP fusion
38	1089	43.8	451	16 AAR70107	TNF-R-GBP 130 fusi
39	1089	43.8	900	16 AAR70103	TNF-R-GBP 130 fusi
40	1088	43.7	1245	16 AAR70105	TNF-R-PL, vlyax Du
41	1088	43.7	1504	16 AAR70105	TNF-R-EBR 175 fusi
42	1005.5	40.4	336	18 AAW33360	TBF(20-190)/hcg-be
43	999	40.2	884	16 AAR70109	TNF-R-GBP 130 fusi
44	979	39.4	285	18 AAW33359	TBF(20-190)/hcg-al
45	946	38.0	168	13 AAR24084	Truncated TNF-alpha

ALIGNMENTS

RESULT 1	
AA10986	
ID	AA10986 standard; Protein; 455 AA.
XX	
AC	AA10986;
XX	
DT	13-MAY-1991 (first entry)
XX	
DE	30kd TNF inhibitor precursor.
XX	
KW	Tumour necrosis factor; inhibitor.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Cleavage-site 40..41
FT	note=" cleavage gives active protein "
XX	
PN	AU9058976-A.
XX	
PD	24-JAN-1991.
XX	
PF	16-JUL-1990; 90AU-0058976.
XX	
PR	07-FEB-1990; 90US-0479661.
PR	18-JUL-1989; 89US-0381080.
PR	11-DEC-1989; 89US-0450329.
XX	
PA	(SYNE-) SYNERGEN INC.
XX	
DR	WPI; 1991-073847/11.
DR	N-PSDB; AAO10883.
XX	

PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
 PT and -beta, useful as therapeutic agent.
 XX
 PS Disclosure: Fig 21: 142pp; English.
 XX
 CC The sequence comprises the entire 30 kD TNF inhibitor. The clone
 CC from which the sequence was deduced was isolated from a cDNA
 CC library prep'd. from RNA form 1937 cells treated with PMA/PMA.
 CC The whole gene can be inserted into expression vectors for prep'n.
 CC of TNF inhibitor for use in the treatment of inflammatory and
 CC degenerative diseases. The active protein is claimed (Claim 8).
 CC See also AAR10984 and AAR11001.
 CC
 XX

Sequence 455 AA:

Query Match 100.0%; Score 2487; DB 12; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.6e-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQKTIHPQNNISICT 60
 DB 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQKTIHPQNNISICT 60
 QY 61 KCHKGTYLYNDCPGQDPTDCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
 DB 61 KCHKGTYLYNDCPGQDPTDCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
 QY 121 RDTVGGCRKNQYRHVWSENLFCFCNCSICLNGTVHLSQCKONTVCTCHAGFFLRNECV 180
 DB 121 RDTVGGCRKNQYRHVWSENLFCFCNCSICLNGTVHLSQCKONTVCTCHAGFFLRNECV 180
 QY 181 SCSNCKKSECTKLCLEPQIENKGTEDSGTTLPLVIFFGCLLSLFLGLMYRYORMK 240
 DB 181 SCSNCKKSECTKLCLEPQIENKGTEDSGTTLPLVIFFGCLLSLFLGLMYRYORMK 240
 QY 241 SKLYSIVCGKSTPEKEGELEGTTRKPLADNPSFPTPGFTPLIGSPVSSFTSSSYT 300
 DB 241 SKLYSIVCGKSTPEKEGELEGTTRKPLADNPSFPTPGFTPLIGSPVSSFTSSSYT 300
 QY 301 PDDCPFAAPRRVAVPYQGADPILATASDPINPDLQKEDSAHKPOSIDTDPATLY 360
 DB 301 PDDCPFAAPRRVAVPYQGADPILATASDPINPDLQKEDSAHKPOSIDTDPATLY 360
 QY 361 AVVENVPPLMKEFYRRLGLSDHEIDRLDELONGRCLEAQSMLATWRRTFRREATLEL 420
 DB 361 AVVENVPPLMKEFYRRLGLSDHEIDRLDELONGRCLEAQSMLATWRRTFRREATLEL 420
 QY 421 IGRVLRMDLGLCLDIEALCGPALPPAPSLR 455
 DB 421 IGRVLRMDLGLCLDIEALCGPALPPAPSLR 455

RESULT 2

ID AAR42059 standard: Protein: 455 AA.

AC AAR42059;

DT 29-APR-1994 (first entry)

DE Lambda derived TNF-R.

XX Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
 XX IL-1R; fusion protein; linker: TNF; IL-1; cachexia; cerebral malaria;
 XX rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
 XX pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
 XX graft versus host disease; sepsis; inflammation; allergy;
 XX autoimmune dysfunction.

OS Homo sapiens.
 OS Lambda-glt0-7ctnfbp.

XX Key Location/Qualifiers
 FH

FT Peptide 1..40
 FT /note= "Signal peptide"
 FT Protein 41..455
 FT /note= "Mature hTNF-R"

MO9319777-A.

14-OCT-1993.

26-MAR-1993; 93MO-US02938.

30-MAR-1992; 92US-0860710.

(IMM) IMMUNEX CORP.

Smith CA;

WPI: 1993-336592/42.

N-PSDB: AAQ49932.

PT New fusion protein tumour necrosis factor and human interleukin-1
 PT receptor - useful in therapy, diagnosis and assays of e.g.
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.

PS Disclosure: Page 57-59; 85pp; English.

CC The sequences given in AAR42058-59 represent human tumour necrosis
 CC factor receptor (TNF-R) and the sequences in AAR42060-61 represent
 CC human interleukin-1 receptor (IL-1R). These sequences were used in
 CC the production of a fusion protein which conformed to one of the
 CC formulae:

TNF-R-linker-TNF-R-linker-IL-1R
 IL-1R-linker-TNF-R-linker-TNF-R or
 TNF-R-linker-TNF-R

CC The linker may comprise 5-100 amino acids selected from Gly, Asp,
 CC Ser, Thr and Ala. These linkers separate the individual moieties
 CC by such a distance that each component of the fusion protein is
 CC capable of folding into the secondary or tertiary structure required
 CC for its biological activity. These fusion proteins may be used in
 CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
 CC particularly in conditions in which both TNF and IL-1 play a causative
 CC role. They may be used to treat cachexia, rheumatoid arthritis,
 CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
 CC cerebral malaria, allograft and xenograft rejection in graft versus
 CC host disease, sepsis, septic shock, inflammation, allergies and
 CC autoimmune dysfunctions.

Sequence 455 AA:

Query Match 100.0%; Score 2487; DB 14; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.6e-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQKTIHPQNNISICT 60
 DB 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQKTIHPQNNISICT 60
 QY 61 KCHKGTYLYNDCPGQDPTDCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
 DB 61 KCHKGTYLYNDCPGQDPTDCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
 QY 121 RDTVGGCRKNQYRHVWSENLFCFCNCSICLNGTVHLSQCKONTVCTCHAGFFLRNECV 180
 DB 121 RDTVGGCRKNQYRHVWSENLFCFCNCSICLNGTVHLSQCKONTVCTCHAGFFLRNECV 180
 QY 181 SCSNCKKSECTKLCLEPQIENKGTEDSGTTLPLVIFFGCLLSLFLGLMYRYORMK 240
 DB 181 SCSNCKKSECTKLCLEPQIENKGTEDSGTTLPLVIFFGCLLSLFLGLMYRYORMK 240
 QY 241 SKLYSIVCGKSTPEKEGELEGTTRKPLADNPSFPTPGFTPLIGSPVSSFTSSSYT 300
 DB 241 SKLYSIVCGKSTPEKEGELEGTTRKPLADNPSFPTPGFTPLIGSPVSSFTSSSYT 300

```

OY 301 PGDCPNFAAPRRVAPPYOGADPIATATASDPINPQKWEBSAHKPOSLDTPDPAITLY 360
DB 301 PGDCPNFAAPRRVAPPYOGADPIATATASDPINPQKWEBSAHKPOSLDTPDPAITLY 360
OY 361 AVVENVPPLRMKEFVRRLGSLDHEIDRLQLONGRCLEAOYSMLATWRRTPREATTLEL 420
DB 361 AVVENVPPLRMKEFVRRLGSLDHEIDRLQLONGRCLEAOYSMLATWRRTPREATTLEL 420
OY 421 LGRVLRMDLGLGLEDIEBALCGPALPPAPSLLR 455
DB 421 LGRVLRMDLGLGLEDIEBALCGPALPPAPSLLR 455

RESULT 3
AAR75084
ID AAR75084 standard; Protein; 455 AA.
XX
AC AAR75084;
XX
DT 19-JAN-1996 (first entry)
XX
DE p55 TNF-R.
XX
KW p55: tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW phorbol myristate acetate; PMA.
XX
OS Homo sapiens.
XX
PH Key
PH Peptide
FT 41..53 Location/Qualifiers
FT /note= "N terminus of soluble p55 TNF-R"
FT Modified-site
FT /note= "glycosylation site"
FT Modified-site
FT /note= "glycosylation site"
FT Modified-site
FT /note= "glycosylation site"
FT Peptide
FT /note= "glycosylation site"
FT Region
FT /note= "peptide used in creation of chimeras"
FT /note= "spacer region"
FT /note= "major C terminus for soluble p55 TNF-R"
FT /note= "essential for shedding reaction"
FT /note= "minor C terminus for soluble p55 TNF-R"
FT Region
FT /note= "transmembrane region"
FT
FT
XX AU9475742-A.
XX
XX 04-MAY-1995.
XX
XX 11-OCT-1994; 94AU-0075742.
XX
XX 12-OCT-1993; 93IL-0107268.
XX
XX (YEDA ) YEDA RES 6 DEV CO LTD.
XX
XX Backin M, Brakebusch C, Varfolomeev E, Wallach D;
XX
XX WPI: 1995-194342/26.
XX
XX N-PSDB; AAG090513.
XX
XX
XX New protease capable of cleaving soluble tumour necrosis factor
XX (TNF) receptor - from cell-bound TNF- receptor, useful for
XX antagonising deleterious effects of TNF.
XX
XX Disclosure: Fig 1; 40pp; English.
XX
XX This sequence represents human p55 tumour necrosis factor (TNF-R).

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CC Expression of this receptor is regulated by shedding of the
CC extracellular receptor fragment. The p55 TNF-R can be shed in response
CC to different inducing agents, e.g. phorbol myristate acetate (PMA),
CC depending on cell type. The only region of the receptor whose structure
CC affects the shedding response is the spacer region (see AAR75012). In the
CC extracellular domain. This region is located close to a site of cleavage
CC of the molecule, and links the Cys rich module to the transmembrane
CC domain. The spacer region of the encoded protein was used to create the
CC chimeras between human p55 TNF-R and murine epidermal growth factor
CC receptor (EGF-R) that are represented by AAR75007-11. This spacer region
CC was subjected to deletion mutations (AAR75013-25) and substitutions
CC (AAR75026-47). Of the spacer region, the most important residues are
CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC important of these. The shedding of the receptor is independent of the
CC side chain identity of these residues, with the exception of a limited
CC dependence on the identity of Val 173. Mutations which alter the
CC conformation of the protein adversely affect the shedding process.
CC The mutations shown in AAR75013-47 were introduced in order to create an
CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
CC inhibitors can be used for enhancing TNF function.
XX
SQ Sequence 455 AA:
Query Match 100.0%; Score 2487; DB 16; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,6e-181;
Matches: 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MGSLTPDILLPLVLELLAVGIRPSGYTGLVPHLGRKREKDSVCPQCKYTHPONNSICCT 60
DB 1 MGSLTPDILLPLVLELLAVGIRPSGYTGLVPHLGRKREKDSVCPQCKYTHPONNSICCT 60
OY 61 KCHKGTLYNDGCGPGDPTDCRCESGSPFASENHLRHCSCKREKMGQVEISSCTVD 120
DB 61 KCHKGTLYNDGCGPGDPTDCRCESGSPFASENHLRHCSCKREKMGQVEISSCTVD 120
OY 121 RDTVCGCRKNQYRHWYSENLFQCFNCSLCNGTVHLSQCKRQNTVCTHAAGFLRENECV 180
DB 121 RDTVCGCRKNQYRHWYSENLFQCFNCSLCNGTVHLSQCKRQNTVCTHAAGFLRENECV 180
OY 181 SCGNCKKSLECTKLCPLQIENVKGTEDSGTTLPLVIFPGICLLSLFGLMYRQRMK 240
DB 181 SCGNCKKSLECTKLCPLQIENVKGTEDSGTTLPLVIFPGICLLSLFGLMYRQRMK 240
OY 241 SKLYSYVCGKSTPEKGELEGTTKPLAPNPSPTPGFTLGFSPVPSSTSSSTYT 300
DB 241 SKLYSYVCGKSTPEKGELEGTTKPLAPNPSPTPGFTLGFSPVPSSTSSSTYT 300
OY 301 PGDCPNFAAPRRVAPPYOGADPIATATASDPINPQKWEBSAHKPOSLDTPDPAITLY 360
DB 301 PGDCPNFAAPRRVAPPYOGADPIATATASDPINPQKWEBSAHKPOSLDTPDPAITLY 360
OY 361 AVVENVPPLRMKEFVRRLGSLDHEIDRLQLONGRCLEAOYSMLATWRRTPREATTLEL 420
DB 361 AVVENVPPLRMKEFVRRLGSLDHEIDRLQLONGRCLEAOYSMLATWRRTPREATTLEL 420
OY 421 LGRVLRMDLGLGLEDIEBALCGPALPPAPSLLR 455
DB 421 LGRVLRMDLGLGLEDIEBALCGPALPPAPSLLR 455

RESULT 4
AAY30934
ID AAY30934 standard; Protein; 455 AA.
XX
XX AAY30934;
XX
XX 18-OCT-1999 (first entry)
XX
XX Human tumour necrosis factor binding protein.
XX
XX Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;

```

KW		anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW		autoimmune glomerulonephritis; cerebral malaria; immune response;
XV		antagonist; diagnosis.
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FH	Peptide	1..29
FT		/label= signal_peptide
FT	Protein	30..435
FT	Modified-site	34
FT		/note= "hypothetical glycosylation site"
FT	Modified-site	125
FT		/note= "hypothetical glycosylation site"
FT	Modified-site	131
FT		/note= "hypothetical glycosylation site"
FT	Region	212..230
FT		/note= "transmembrane region"
FT	Modified-site	250
FT		/note= "hypothetical glycosylation site"
FN		
XX	EP93j9121-A2.	
XX		
PD	01-SEP-1999.	
PX		
PF	31-AUG-1990;	90EP-0116707.
PR	20-APR-1990;	90CH-0001347.
PR	12-SEP-1989;	89CH-0003319.
PR	08-MAR-1990;	90CH-0000746.
XX		
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.	
XX		
P1	Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Ioetscher H;	
P1	Schlaeger E;	
XX		
DR	WP1: 1999-480840/41.	
DR	N-PADB: AAZ09170.	
XX		
PT	New insoluble proteins, and fragments, that bind to tumor necrosis factor, used to treat e.g. septic shock or cerebral malaria	
PS	Claim 4a; Fig 1; 25pp; German.	
CC	This invention describes novel homogeneous insoluble proteins (I), their (II)insoluble fragments (Ia) and their salts that can bind tumour necrosis factor (TNF). The products of the invention have anti-inflammatory and antimalarial activity. (I) and (Ia) are used (I) to treat diseases in which TNF is involved (e.g. septic shock, autoimmune glomerulonephritis, cerebral malaria, immune responses and inflammation), (II) to purify TNF, (III) to identify TNF antagonists and (IV) for diagnostic determination of TNF in body fluids. Antibodies raised against (I) are used for affinity purification of (I). This sequence represents a tumour necrosis factor binding protein described in the method of the invention.	
CC		
CC		
CC		
CC		
CC		
CC		
CC		
CC		
CQ	Sequence	455 AA:
SQ		
	Query Match	100.0%; Score 2487; DB 20; Length 455;
	Best Local Similarity	100.0%; Pred. No. 4,6e+181;
	Matches	455; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 MGSLTVPDLLPLVLLELLVGIVPGSVIGLVPHLGDREKRDSVCPOGXIHPONNISCTG	60
DB	1 MGSLTPDPLLPLVLELVGLVPGVIGLVPHLDGREKRDSSVCPOGYTHPQNNSICTG	60
OY	61 KCHHGTYLYNDCPPGGOTDCECGSGSFASENHLRHCLSCSKCKEKMGQVEISSCTVD	120
DB	61 KCHHGTYLYNDCPPGGOTDCECGSGSFASENHLRHCLSCSKCKEKMGQVEISSCTVD	120
OY	121 RDVTGGCGRKNKYRIHWSENLFQCFCNFCSICLNSTVHLSOEGKONTWCCTAGAFILRENECV	180
DB	121 RDVTGGCGRKNKYRIHWSENLFQCFCNFCSICLNSTVHLSOEGKONTCCTAGAFILRENECV	180
OY	121 RDVTGGCGRKNKYRIHWSENLFQCFCNFCSICLNSTVHLSOEGKONTWCCTAGAFILRENECV	180
DB	121 RDVTGGCGRKNKYRIHWSENLFQCFCNFCSICLNSTVHLSOEGKONTCCTAGAFILRENECV	180

[illegible]

CC	RESULT 5
CC	AAB36266
CC	AAB36266 standard; Protein; 455 AA.
CC	
CC	AAB36266;
CC	
CC	20-FEB-2001 (first entry)
CC	
CC	Human tumour necrosis factor receptor 1.
CC	
CC	Human; death domain containing receptor; DR3-V1; cancer;
CC	autoimmune disorder; inflammation; cardiovascular disorder; infection;
CC	neurodegenerative disease; angiogenesis.
CC	
CC	Homo sapiens.
CC	
CC	WO2000064465-A1.
CC	
CC	02-NOV-2000.
CC	
CC	21-APR-2000; 2000WO-US10741.
CC	
CC	22-APR-1999; 99US-0130488.
CC	
CC	28-MAY-1999; 99US-0136741.
CC	
CC	(HUMA-) HUMAN GENOME SCI INC.
CC	(UNMT) UNIV MICHIGAN.
CC	(YUGG/) YU G.
CC	(NIJJ/) NI J.
CC	(GENT/) GENTZ R L.
CC	(DILL/) DILLON P J.
CC	(DIXI/) DIXIT V M.
CC	
CC	YU G, NI J, Gentz RL, Dillon PJ, Dixit VM;
CC	
CC	PMI; 2000-687263/67.
CC	
CC	Treating graft-versus-host disease, cancer, immunodeficiency or an
CC	autoimmune disease comprising administering an antibody to Death Domain
CC	Containing Receptor proteins and a second therapeutic agent -
CC	
CC	Disclosure; Fig 3; 273pp; English.
CC	
CC	The present invention provides the protein and coding sequences for two
CC	death domain containing receptors, designated DR3 and DR3-V1. These
CC	receptors are involved in apoptosis, and the sequences given can be used
CC	in the treatment of cancers, infections, cardiovascular disorders such as
CC	arhythmias, ischemia, aneurysms, arterial occlusive diseases, embolisms
CC	and congenital heart defects, neurodegenerative diseases including
CC	Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
CC	sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
CC	

CC and to promote angiogenesis and wound healing.

XX Sequence 455 AA;

Query Match 100.0%; Score 2487; DB 21; Length 455;
Best local similarity 100.0%; Pred. No. 4,6e-181;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGISTVPDLLPLVLELLVGIYPSGVIIGLPHLGDREKRDVCPQCKYIHPONNISICT 60
DB 1 MGISTVPDLLPLVLELLVGIYPSGVIIGLPHLGDREKRDVCPQCKYIHPONNISICT 60
OY 61 KCHKGTLYNDGPGPGDPTDCRECESSGFTASNNHLRHLCSCSKCKREKQVEISSCTVD 120
DB 61 KCHKGTLYNDGPGPGDPTDCRECESSGFTASNNHLRHLCSCSKCKREKQVEISSCTVD 120
OY 121 RDIVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
DB 121 RDIVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
OY 181 SCGNCKKSLLECTKLCPLQIENVKGTEDSGTTLVLLPVIFGCLLSLFTGLMYRYQRMK 240
DB 181 SCGNCKKSLLECTKLCPLQIENVKGTEDSGTTLVLLPVIFGCLLSLFTGLMYRYQRMK 240
OY 241 SKIYIVCGKSTPEKEGELEGGTTTKPLAPNPSPTPGFTLGFSPVPSSTTSSTYT 300
DB 241 SKIYIVCGKSTPEKEGELEGGTTTKPLAPNPSPTPGFTLGFSPVPSSTTSSTYT 300
OY 301 PGDCPNFAAPRRREYAPPYGADPILATALASDPINPDLQKWEBSAHKPOSLDTPDDPATLY 360
DB 301 PGDCPNFAAPRRREYAPPYGADPILATALASDPINPDLQKWEBSAHKPOSLDTPDDPATLY 360
OY 361 AVVENPPLPWLKKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRTPRREATLEL 420
DB 361 AVVENPPLPWLKKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRTPRREATLEL 420
OY 421 LGRVLRMDMLGCLLEDEIEALCGPALPPAPSLLR 455
DB 421 LGRVLRMDMLGCLLEDEIEALCGPALPPAPSLLR 455

RESULT 6

AAB37800 standard; Protein; 455 AA.

AC AAB37800;
DT 23-FEB-2001 (first entry)

DE Human tumour necrosis factor p55 receptor.

XX Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
KW p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
KW immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
KW chronic myelogenous leukemia; inflammatory bowel disease.

OS Homo sapiens.

XX MO200064479-A1.

PD 02-NOV-2000.

PF 26-APR-2000; 2000WO-US11700.

PR 27-APR-1999; 99US-0301274.

PA (ANTI-) ANTIBODY SYSTEMS INC.

PI Fredeking TM, Ignatyev GM;

DR WPI: 2000-679646/66.

XX Novel compositions comprising tetracycline or tetracycline-like
PT compounds for the treatment and/or prevention of acute inflammatory
PT responses and diseases, e.g. septic shock and immune complex-induced
PT colitis -
PS Disclosure: Page 167-169; 183pp; English.

CC The present sequence is given in a specification relating to novel
CC compositions and methods containing tetracycline or tetracycline-like
CC compounds for treating and/or preventing acute inflammatory responses and
CC diseases. Such diseases include acute inflammatory conditions associated
CC with viral haemorrhagic diseases (including diseases caused by
CC Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),
CC parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
CC disorders, acute cardiovascular events, chronic myelogenous leukemia and
CC transplanted bone marrow-induced graft-versus-host disease, septic shock,
CC immune complex-induced colitis, cerebrospinal fluid inflammation,
CC systemic sclerosis, inflammatory response associated with trauma,
CC multiple inflammatory response syndrome (SIRS), adult respiratory
CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
CC and Crohn's disease.

SO Sequence 455 AA;

Query Match 100.0%; Score 2487; DB 21; Length 455;
Best local similarity 100.0%; Pred. No. 4,6e-181;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGISTVPDLLPLVLELLVGIYPSGVIIGLPHLGDREKRDVCPQCKYIHPONNISICT 60
DB 1 MGISTVPDLLPLVLELLVGIYPSGVIIGLPHLGDREKRDVCPQCKYIHPONNISICT 60
OY 61 KCHKGTLYNDGPGPGDPTDCRECESSGFTASNNHLRHLCSCSKCKREKQVEISSCTVD 120
DB 61 KCHKGTLYNDGPGPGDPTDCRECESSGFTASNNHLRHLCSCSKCKREKQVEISSCTVD 120
OY 121 RDIVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
DB 121 RDIVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
OY 181 SCGNCKKSLLECTKLCPLQIENVKGTEDSGTTLVLLPVIFGCLLSLFTGLMYRYQRMK 240
DB 181 SCGNCKKSLLECTKLCPLQIENVKGTEDSGTTLVLLPVIFGCLLSLFTGLMYRYQRMK 240
OY 241 SKIYIVCGKSTPEKEGELEGGTTTKPLAPNPSPTPGFTLGFSPVPSSTTSSTYT 300
DB 241 SKIYIVCGKSTPEKEGELEGGTTTKPLAPNPSPTPGFTLGFSPVPSSTTSSTYT 300
OY 301 PGDCPNFAAPRRREYAPPYGADPILATALASDPINPDLQKWEBSAHKPOSLDTPDDPATLY 360
DB 301 PGDCPNFAAPRRREYAPPYGADPILATALASDPINPDLQKWEBSAHKPOSLDTPDDPATLY 360
OY 361 AVVENPPLPWLKKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRTPRREATLEL 420
DB 361 AVVENPPLPWLKKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRTPRREATLEL 420
OY 421 LGRVLRMDMLGCLLEDEIEALCGPALPPAPSLLR 455
DB 421 LGRVLRMDMLGCLLEDEIEALCGPALPPAPSLLR 455

RESULT 7

AAB26984 standard; Protein; 455 AA.

XX AAB26984;

DT 02-FEB-2001 (first entry)

DE Human TNFR 1.

KW Human; TNFR 1; tumour necrosis factor; TNF receptor; immunosuppressive;

KM antiinflammatory; cardiant; antiaesthetic; antidiabetic; antiallergic;
 KM antitubercic; antitubercic; anti-HIV; anticonvulsant; cyostatic;
 KM neuroprotective; gene therapy; Death Domain Containing Receptor 6;
 KM common variable immunodeficiency; X-linked agammaglobulinemia;
 KM severe combined immunodeficiency; Wiskott-Aldrich syndrome;
 KM autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
 KM multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
 KM cardiovascular disease; neurological disease; protein coordinate data.
 XX
 OS Homo sapiens.
 PN WO200056862-A1.
 XX
 XX 28-SEP-2000.
 PD
 XX 16-MAR-2000; 2000WO-US06831.
 PF
 XX 24-MAR-1999; 99US-0126019.
 PR 14-MAY-1999; 99US-0134220.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ni J, Gentz RL, Yu G, Fan P;
 PI
 XX WPI: 2000-594575/56.
 DR
 XX Nucleic acid molecule encoding a human tumor necrosis factor receptor,
 PT known as TR9, useful for treating, preventing and diagnosing severe
 PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
 PT and cancer -
 XX
 PS Disclosure: Fig 2; 220pp; English.
 XX
 XX The present sequence is TNFR 1, a member of the tumour necrosis factor
 CC receptor family. A novel human tumour necrosis factor receptor,
 CC designated TR9, has been isolated. The TR9 receptor is also known as
 CC Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or
 CC agonists are useful for treating, preventing or diagnosing common
 CC variable immunodeficiency, X-linked agammaglobulinemia, severe combined
 CC immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such
 CC as Rheumatoid arthritis, Wiskott-Aldrich syndrome, multiple sclerosis,
 CC diabetes mellitus and asthma), HIV infection, epilepsy, cancer,
 CC cardiovascular diseases and other neurological diseases.
 CC
 SO Sequence 455 AA;
 Query Match 100.0%; Score 2487; DB 21; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.6e-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 AVENVPLRMKEFVRLGSDHEIDRLQNGRCLEA9YSMLATWRRTPREATLEL 420
 DB 361 AVENVPLRMKEFVRLGSDHEIDRLQNGRCLEA9YSMLATWRRTPREATLEL 420
 QY 421 LGRVLRMDLGLGEDIIEFALCPALPPAPSLR 455
 DB 421 LGRVLRMDLGLGEDIIEFALCPALPPAPSLR 455
 RESULT 8
 AAB23446
 ID AAB23446 standard; Protein; 455 AA.
 XX
 XX AAB23446;
 AC
 XX 12-JAN-2001 (first entry)
 DT
 XX Human tumour necrosis factor receptor 1 protein.
 DE
 XX TNFR1; tumour necrosis factor receptor; polymorphism; human;
 KW tumour; cancer; apoptosis; bacterial infection.
 KM
 XX Homo sapiens.
 OS
 XX WO200050436-A1.
 PN
 XX 31-AUG-2000.
 PD
 XX 23-FEB-2000; 2000WO-US04606.
 PF
 XX 23-FEB-1999; 99US-0121314.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA (NAND/) NANDABALAN K.
 PA (SCHU/) SCHULZ V P.
 PA (STEP/) STEPHENS J C.
 PA (CHEW/) CHEW A.
 XX
 XX NANDABALAN K, Schulz VP, Stephens JC, Chew A;
 DR WPI: 2000-543909/49.
 DR N-PSDB: AAA95105.
 XX
 XX Polynucleotides comprising polymorphic variants of a reference sequence
 PT for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
 PT biological function of TNFR1 and identifying drugs targeting the
 PT protein for treating disorders -
 XX
 PS Claim 10; Fig 5; 79pp; English.
 XX
 XX The present invention relates to polymorphic variants of the tumour
 CC necrosis factor receptor 1 (TNFR1) gene. The present sequence is
 CC the TNFR1 protein. The sequence of the whole gene is given in AAA95102,
 CC AAA95103 and AAA95104. The polymorphisms were identified by amplifying
 CC and sequencing regions of the gene. Twelve polymorphic loci
 CC were discovered. Of these twelve polymorphisms, four can cause a
 CC change in the TNFR1 protein. The TNFR1 polymorphisms may be useful
 CC for studying the biological function of TNFR1 as well as for
 CC identifying drugs targeting the protein for treatment of disorders
 CC related to its abnormal expression or function such as tumours,
 CC apoptosis related disorders and bacterial infection.
 CC
 SO Sequence 455 AA;
 Query Match 100.0%; Score 2487; DB 21; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.6e-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 KCHKGYLYNDGPGDPTDCRCESGSPFTASENHLRHCLSCSKCKREKMOVEISSCTVD 120
 DB 61 KCHKGYLYNDGPGDPTDCRCESGSPFTASENHLRHCLSCSKCKREKMOVEISSCTVD 120
 QY 121 RDVYCGCRKQYRHYWSENLFQCFNCSLCNGVHLSQCKOKNTVCTCHAGFFLRENECV 180
 DB 121 RDVYCGCRKQYRHYWSENLFQCFNCSLCNGVHLSQCKOKNTVCTCHAGFFLRENECV 180
 QY 181 SCGNCKKSLCCTKLCPLQIENKGTEDSGTTLPLVIFPGCLLSLFTGLMYRYQRMK 240
 DB 181 SCGNCKKSLCCTKLCPLQIENKGTEDSGTTLPLVIFPGCLLSLFTGLMYRYQRMK 240
 QY 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 DB 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 QY 301 PGDCPNFAAPRREYAPPYQADPILATLASDPIPNPLOKWEBSAHKPOSLDTPDPTLY 360
 DB 301 PGDCPNFAAPRREYAPPYQADPILATLASDPIPNPLOKWEBSAHKPOSLDTPDPTLY 360
 QY 361 AVVENVPPLRMKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRTPPREATLEL 420
 DB 361 AVVENVPPLRMKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRTPPREATLEL 420
 QY 421 LGRVLRDMDLGCLDEIEALCGPALPPAPSLLR 455
 DB 421 LGRVLRDMDLGCLDEIEALCGPALPPAPSLLR 455

RESULT 9

ID AAB01336 standard; Protein; 455 AA.
 XX AAB01336;
 XX 25-SEP-2000 (first entry)
 XX TNF-R1 death receptor.
 DE TNF-R1 death receptor.
 XX UL144; death receptor; apoptosis; programmed cell death; FAS;
 KM TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
 KM human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200034335-A2.
 XX 15-JUN-2000.
 PD 03-DEC-1999; 99WO-US26035.
 PF 04-DEC-1998; 98US-0205018.
 PR (SCHE) SCHERING CORP.
 XX Leong C, Phillips JH;
 PI WPI; 2000-42393/36.
 DR Purified or recombinant polypeptide for modulating apoptosis comprises
 XX a sequence which binds to an antibody specific for UL144 or its
 PT fragments
 PS Disclosure; Page 65-67; 76pp; English.
 CC A pure or recombinant polypeptide which binds to a polyclonal antibody
 CC specific for the mature UL144 is useful for screening molecules which
 CC block induction of apoptosis or interfere with antiapoptotic activity.
 CC The polypeptide is also useful for modulating apoptosis and useful in
 CC treatment of conditions associated with abnormal physiology or
 CC development, such as cancer or degenerative conditions and for
 CC regulation of viral infection and replication. At least five
 CC different death receptors are known, which include the CD95

CC (Fas/Apo-1), the TNF receptor-1, TNF receptor apoptosis-mediated
 CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related
 CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
 XX Sequence 455 AA;
 SO Query Match 100.0%; Score 2487; DB 21; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4, 6e-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDLPLVLELLVIGTIPSGVIGLVPHLGDEKRDVCPQKTYHPONNSICTT 60
 DB 1 MGISTVPDLPLVLELLVIGTIPSGVIGLVPHLGDEKRDVCPQKTYHPONNSICTT 60
 QY 61 KCHKGYLYNDGPGDPTDCRCESGSPFTASENHLRHCLSCSKCKREKMOVEISSCTVD 120
 DB 61 KCHKGYLYNDGPGDPTDCRCESGSPFTASENHLRHCLSCSKCKREKMOVEISSCTVD 120
 QY 121 RDVYCGCRKQYRHYWSENLFQCFNCSLCNGVHLSQCKOKNTVCTCHAGFFLRENECV 180
 DB 121 RDVYCGCRKQYRHYWSENLFQCFNCSLCNGVHLSQCKOKNTVCTCHAGFFLRENECV 180
 QY 181 SCGNCKKSLCCTKLCPLQIENKGTEDSGTTLPLVIFPGCLLSLFTGLMYRYQRMK 240
 DB 181 SCGNCKKSLCCTKLCPLQIENKGTEDSGTTLPLVIFPGCLLSLFTGLMYRYQRMK 240
 QY 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 DB 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 QY 301 PGDCPNFAAPRREYAPPYQADPILATLASDPIPNPLOKWEBSAHKPOSLDTPDPTLY 360
 DB 301 PGDCPNFAAPRREYAPPYQADPILATLASDPIPNPLOKWEBSAHKPOSLDTPDPTLY 360
 QY 361 AVVENVPPLRMKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRTPPREATLEL 420
 DB 361 AVVENVPPLRMKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRTPPREATLEL 420
 QY 421 LGRVLRDMDLGCLDEIEALCGPALPPAPSLLR 455
 DB 421 LGRVLRDMDLGCLDEIEALCGPALPPAPSLLR 455

RESULT 10

ID AAB86817 standard; Protein; 455 AA.
 XX AAB86817;
 XX 12-NOV-2001 (first entry)
 DE Human TNFBP-associated protein #1.
 XX TNF; tumor necrosis factor binding protein; TNFBP; treatment;
 KM insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
 KM anti-protozoal; treatment; meningococcal sepsis; cerebral malaria;
 KM autoimmune glomerulonephritis.
 XX Homo sapiens.
 OS Homo sapiens.
 XX EP1132471-A2.
 PD 12-SEP-2001.
 PF 31-AUG-1990; 2001EP-0108117.
 PR 12-SEP-1989; 89CH-00003319.
 PR 08-MAR-1990; 90CH-0000746.
 PR 20-APR-1990; 90CH-0001347.
 PR 31-AUG-1990; 90EP-0116707.
 PR 31-AUG-1990; 99EP-0100703.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
 PI Schlaefer E;
 XX WPI: 2001-559312/63.
 DR N-PSDB; AAH48859.
 XX
 PT New homogeneous, insoluble proteins that bind tumor necrosis factor
 PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
 XX
 PS Claim 4a; Fig 1; 26pp; German.
 CC This invention describes novel insoluble proteins (I), also their
 CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
 CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
 CC invention have antiinflammatory, immunosuppressive, antibacterial,
 CC antiparasitic activity. (I), and related recombinant proteins, are used
 CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
 CC sepsis; development of autoimmune glomerulonephritis and cerebral
 CC malaria. Also (I), or antibodies specific for them, are used for
 CC diagnostic determination of TNF in body fluids, for affinity purification
 CC of TNF and for identifying (ant)agonists of TNF. This sequence represents
 CC a human TNF binding protein described in the method of the invention.
 XX
 SQ Sequence 455 AA;

Query Match 100.0%; Score 2487; DB 22; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4,66-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGISTVPDLLPLVLLELVGTVPSGVIGLVPHLGDREKRDVCPGKTIHQNNISICT 60
DB 1 MGISTVPDLLPLVLLELVGTVPSGVIGLVPHLGDREKRDVCPGKTIHQNNISICT 60
QY 61 KCHKGTLYLNDGPGQDPTDCECESGSFTASENHLRHLCSCSKCKEKGVEISSCTVD 120
DB 61 KCHKGTLYLNDGPGQDPTDCECESGSFTASENHLRHLCSCSKCKEKGVEISSCTVD 120
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSCEQKONTVCTCHAGFFLENECV 180
DB 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSCEQKONTVCTCHAGFFLENECV 180
QY 181 SCSNCKKSLCTKRLCLPQLENVKGTEDSGTYVLLPLVIFGGLCLSLFTGLMYRQRMK 240
DB 181 SCSNCKKSLCTKRLCLPQLENVKGTEDSGTYVLLPLVIFGGLCLSLFTGLMYRQRMK 240
QY 241 SKLYSIVCGKSTPEKEGELGTTTRPLADNPSFSPPTGFTPLGFSVPSSFTSSSTYT 300
DB 241 SKLYSIVCGKSTPEKEGELGTTTRPLADNPSFSPPTGFTPLGFSVPSSFTSSSTYT 300
QY 301 PDDCFNFAAPRRVAPRYGADPILATALASDPINPDLQKWDSDAHKPOSLOTDPAATLY 360
DB 301 PDDCFNFAAPRRVAPRYGADPILATALASDPINPDLQKWDSDAHKPOSLOTDPAATLY 360
QY 361 AVVENVPPLRMKEFVRRLGLSDHEIDRLONGRCLEAEGSMLATWRRRTPRREATLEL 420
DB 361 AVVENVPPLRMKEFVRRLGLSDHEIDRLONGRCLEAEGSMLATWRRRTPRREATLEL 420
QY 421 IGRVLRDMDLGLCLDIEBALGPAALPPAPSLIR 455
DB 421 IGRVLRDMDLGLCLDIEBALGPAALPPAPSLIR 455

```

RESULT 11

AAAB36697
 ID AAAB36697 standard; Protein; 455 AA.

XX AAAB36697;

XX 15-MAR-2001 (first entry)

XX Human tumour necrosis factor receptor TNFR1 protein SMO ID NO:3.

KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nontropic;
 KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
 KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;
 KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
 KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
 KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
 KW apoptotic cell death related disease; autoimmune disorder;
 KW cardiovascular disorder; viral infection.
 XX
 OS Homo sapiens.
 PN WO200071150-A1.
 XX
 PD 30-NOV-2000.
 XX
 PD 18-MAY-2000; 2000WO-US13515.
 XX
 PD 20-MAY-1999; 99US-0135164.
 XX
 PI (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Wei Y, Ruben SM, Gentz RL, NI J;
 XX
 DR WPI: 2001-041051/05.
 XX
 PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor
 PT necrosis factor receptor 5, useful in the diagnosis, treatment or
 PT prevention of cancer, autoimmune disorders and viral infection -
 XX
 PS Disclosure; Fig 2; 285pp; English.

The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytosolic, immunosuppressive, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention.

SO Sequence 455 AA;

Query Match 100.0%; Score 2487; DB 22; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4,66-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGISTVPDLLPLVLLELVGTVPSGVIGLVPHLGDREKRDVCPGKTIHQNNISICT 60
DB 1 MGISTVPDLLPLVLLELVGTVPSGVIGLVPHLGDREKRDVCPGKTIHQNNISICT 60
QY 61 KCHKGTLYLNDGPGQDPTDCECESGSFTASENHLRHLCSCSKCKEKGVEISSCTVD 120
DB 61 KCHKGTLYLNDGPGQDPTDCECESGSFTASENHLRHLCSCSKCKEKGVEISSCTVD 120
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSCEQKONTVCTCHAGFFLENECV 180
DB 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSCEQKONTVCTCHAGFFLENECV 180
QY 181 SCSNCKKSLCTKRLCLPQLENVKGTEDSGTYVLLPLVIFGGLCLSLFTGLMYRQRMK 240

```


|||||
Db 181 SCSNCKSLCTKLCPLQIENVKGTEDSGTTVLPVIFFGCLLSLFLGLMRYORWK 240
QY 241 SKLYSIVCGKSTPEKEGELGGTTTKPLAPNPSFSPTGFTPTLGFSPVPSSTFTSSSTYT 300
Db 241 SKLYSIVCGKSTPEKEGELGGTTTKPLAPNPSFSPTGFTPTLGFSPVPSSTFTSSSTYT 300
QY 301 PGDCPNFAAPRRREVAPPYQAGADPLATATLASDPIPNPLQKWEDSAHKPQSLDTPDDPATLY 360
Db 301 PGDCPNFAAPRRREVAPPYQAGADPLATATLASDPIPNPLQKWEDSAHKPQSLDTPDDPATLY 360
QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLLEQNGRCLEAQSMLATYRRRTPREATLEL 420
Db 361 AVVENVPPLMKKEFVRRLGSDHEIDRLLEQNGRCLEAQSMLATYRRRTPREATLEL 420
QY 421 LGRVLRMDLLGCLLEIDIEEALCGPALPAPPSLLR 455
Db 421 LGRVLRMDLLGCLLEIDIEEALCGPALPAPPSLLR 455
RESULT 12
AAB37677
ID AAB37677 standard; protein; 455 AA.
XX
AC AAB37677;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human 30 kDa TNF inhibitor precursor.
XX
KM TNF inhibitor; antinflammatory; Tumour Necrosis Factor; Interleukin;
KW IL-1; Inflammatory disease; degenerative disease; human.
XX
OS Homo sapiens.
XX
PN US6143866-A.
XX
PD 07-NOV-2000.
XX
PF 19-JAN-1995; 95US-0375242.
XX
PR 19-JUL-1990; 90US-0555274.
PR 09-JUL-1993; 93US-0090366.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
XX
PA (AMGE-) AMGEN INC.
XX
PI Squites C, King MW, Hale KK, Brewer MT, Thompson RC;
PI Vanderslice RW, Vannice J, Kohno T;
XX
DR WPI: 2001-006443/01.
DR N-PSDB; AAC83946.
XX
PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF -
XX
PS Example 6; Fig 21; 82pp; English.
XX
CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC novel TNF inhibitors of the present invention are useful as therapeutic
CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC for treating inflammatory and degenerative diseases mediated by TNF. The
CC present sequence is the precursor for 30 kDa TNF inhibitor. The 30 kDa
CC TNF inhibitor can inhibit TNF alpha.
XX
SQ Sequence 455 AA;
Query Match 100.0%; Score 2487; DB 22; Length 455;

Best Local Similarity 100.0%; Pred. No. 4 6e-181;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGISTVPDLLPLVLELLVIGVPSGVIGLYPHLGDEKRDVSCPOGKYTHPONNSICCT 60
Db 1 MGISTVPDLLPLVLELLVIGVPSGVIGLYPHLGDEKRDVSCPOGKYTHPONNSICCT 60
QY 61 KCHKGTLYNDPCPGQDTCRECESSFTASENHLRHCLSCSKRKEKMGVEISSCTVD 120
Db 61 KCHKGTLYNDPCPGQDTCRECESSFTASENHLRHCLSCSKRKEKMGVEISSCTVD 120
QY 121 RDTVCCGRKKQRYRYSENLPCQFCNCLCNGYVHLSQCKQNTVCTCHAGFPLRENECV 180
Db 121 RDTVCCGRKKQRYRYSENLPCQFCNCLCNGYVHLSQCKQNTVCTCHAGFPLRENECV 180
QY 181 SCSNCKSLCTKLCPLQIENVKGTEDSGTTVLPVIFFGCLLSLFLGLMRYORWK 240
Db 181 SCSNCKSLCTKLCPLQIENVKGTEDSGTTVLPVIFFGCLLSLFLGLMRYORWK 240
QY 241 SKLYSIVCGKSTPEKEGELGGTTTKPLAPNPSFSPTGFTPTLGFSPVPSSTFTSSSTYT 300
Db 241 SKLYSIVCGKSTPEKEGELGGTTTKPLAPNPSFSPTGFTPTLGFSPVPSSTFTSSSTYT 300
QY 301 PGDCPNFAAPRRREVAPPYQAGADPLATATLASDPIPNPLQKWEDSAHKPQSLDTPDDPATLY 360
Db 301 PGDCPNFAAPRRREVAPPYQAGADPLATATLASDPIPNPLQKWEDSAHKPQSLDTPDDPATLY 360
QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLLEQNGRCLEAQSMLATYRRRTPREATLEL 420
Db 361 AVVENVPPLMKKEFVRRLGSDHEIDRLLEQNGRCLEAQSMLATYRRRTPREATLEL 420
QY 421 LGRVLRMDLLGCLLEIDIEEALCGPALPAPPSLLR 455
Db 421 LGRVLRMDLLGCLLEIDIEEALCGPALPAPPSLLR 455
RESULT 13
AAB81649
ID AAB81649 standard; protein; 455 AA.
XX
AC AAB81649;
XX
DT 26-SEP-2002 (first entry)
XX
DE Human tumour necrosis factor alpha protein SEQ ID NO:3.
XX
KM Human: apoptosis inducing molecule II; AIM II; cytostatic; antiarthritic;
KM antitumour; immunosuppressive; antibacterial; antinflammatory;
KM immunomodulator; vasotropic; protozoacide; cerebroprotective; neoplasia;
KM haematopoiesis regulator; lymphadenopathy; rheumatoid arthritis; HIV;
KM autoimmune disease; graft versus host disease; restenosis; septic shock;
KM cytokine adjuvant; costimulatory molecule; inflammation; bone resorption;
KM cerebral malaria; cachexia.
XX
OS Homo sapiens.
XX
PN US2002064869-A1.
XX
PD 30-MAY-2002.
XX
PF 20-FEB-1998; 98US-0027287.
XX
PR 22-MAR-1996; 96US-013923P.
PR 31-OCT-1996; 96US-030157P.
PR 21-MAR-1997; 97US-0822953.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ebner R, Yu G, Ruben SM, Ullrich S;
XX
DR WPI: 2002-556723/59.
XX
PT Novel apoptosis inducing molecule II polypeptide useful for treating

PT lymphadenopathy, autoimmune disease, graft versus host disease and to
PT inhibit neoplasia such as tumor cell growth -
PS Disclosure; Fig 2A-C; 79pp; English.
XX
XX
XX The present invention describes human apoptosis inducing molecule II
CC (AIM II) protein (I). (I) has cytostatic, antiarthritic, antirheumatic,
CC immunosuppressive, antibacterial, antiinflammatory, immunomodulator,
CC vasculoprotective and cerebroprotective activities, and can be
CC used as an inhibitor of neoplasia and a haematopoiesis regulator.
CC AIM II polypeptides can be used for treating lymphadenopathy, rheumatoid
CC arthritis, autoimmune disease and graft versus host disease. AIM II
CC polypeptides may also be used to treat diseases which require growth
CC promotion activity for e.g. restenosis and are employed to regulate
CC haematopoiesis in endothelial cell development. The polypeptide may act
CC as cytokine adjuvant or costimulatory molecule. Cells expressing the
CC polypeptide are useful for identifying compounds capable of enhancing or
CC inhibiting a cellular response induced by AIM II. Antagonists of AIM II
CC are useful to prevent septic shock, inflammation, cerebral malaria,
CC activation of the HIV virus, graft-host rejection, bone resorption and
CC cachexia. AIM II polynucleotides are useful for the diagnosis and
CC treatment of disorders of cells, tissues and organisms, for chromosome
CC identification, and to detect complementary polynucleotides. Detection
CC of a mutated form of AIM II associated with a dysfunction provides a
CC diagnostic tool for autoimmune diseases. The present sequence is given
CC in comparison with human AIM II in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 455 AA;
Query Match 100.0%; Score 2487; DB 23; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.6e-181;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLPLVLELLVGIYPSGVILVPHLGDREKRDVCPGKGIYHPQNNISICT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVILVPHLGDREKRDVCPGKGIYHPQNNISICT 60
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DB 121 RPTVCGCRKNQYRHYWSENLFOCFNCISLCNGTVHLSCEKQNTVCTCHAGFFLRNECV 180
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DB 181 SCSNCKKSLCTKCLCPQLENVKGTEDSGTYLLPLVIFGCLSLTGLMYRQRMK 240
QY 241 SKLYSTIVCGKSTPEKEGELGTTTTPKLANPFSPPGFTPLGSPVSSFTSSSTYT 300
DB 241 SKLYSTIVCGKSTPEKEGELGTTTTPKLANPFSPPGFTPLGSPVSSFTSSSTYT 300
QY 301 PDDCNFAAPRREVAAPPYOGADPILATALASPIPNPLQKWDKSAHKPSLTDTPATLY 360
DB 301 PDDCNFAAPRREVAAPPYOGADPILATALASPIPNPLQKWDKSAHKPSLTDTPATLY 360
QY 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQNGRCLREAOYSMLATWRRTTFRREATTEL 420
DB 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQNGRCLREAOYSMLATWRRTTFRREATTEL 420
QY 421 LGRVLRDMDDLGLCEDIEALCGPALPAPSLR 455
DB 421 LGRVLRDMDDLGLCEDIEALCGPALPAPSLR 455
RESULT 14
AAU75064
ID AAU75064 standard; Protein: 455 AA.
XX
XX
AC AAU75064;
XX

DT 23-APR-2002 (first entry)
XX
XX Human tumour necrosis factor alpha (TNF alpha) receptor protein.
DE
XX
XX TNF alpha: apoptosis; tumour; death domain receptor ligand;
KW dipteropod triepoxide; cytostatic activity; c-IAP2; c-IAP1;
KW carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma;
KW neurologic malignancy; haematological malignancy; lichen planus;
KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
KW discoid lupus erythematosus; human; receptor; TNF-R1.
XX
XX Homo sapiens.
OS
XX
XX US6329148-B1.
PN
XX
XX 11-DEC-2001.
PD
XX
XX 15-FEB-2000; 2000US-0505250.
PF
XX
XX 16-FEB-1999; 99US-120313P.
PR
XX
XX 20-AUG-1999; 99US-149989P.
PR
XX
XX (STRD) UNITV LELAND STANFORD.
PA
XX
XX Rosen GD, Kao P;
PI
XX
XX MPI: 2002-121125/16.
DR
XX
XX N-PSDB; ABK13194.
DR
XX
XX Use of a synergistic combination of death domain receptor ligands and
PT dipteropod triepoxides for killing of tumour cells -
PT
XX
XX Disclosure; Column 23-28; 20pp; English.
PS
XX
XX This invention relates to a novel method for enhanced killing of tumour
CC cells comprising contacting a tumour cell with a synergistic
CC combination of a death domain receptor ligand and a dipteropod
CC triepoxide. This method has cytostatic activity and works by blocking
CC TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the
CC invention may be used for treating tumours, particularly solid tumours,
CC e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma
CC also neurologic malignancies, haematological malignancies, e.g.
CC non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant
CC cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma,
CC lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia,
CC bullous pemphigoid, discoid lupus erythematosus, lichen planus. The
CC combination may be administered with other active agents, e.g. anti-
CC metastatic, anti-tumour or anti-angiogenic agents. The potent synergy
CC between the dipteropod and the death domain ligands allows increased
CC killing at equivalent or lower doses, and can sensitize otherwise
CC resistant cells. This sequence represents the human tumour necrosis
CC factor alpha receptor (TNF-R1) protein. TNF-R1 is a death domain
CC receptor used in the used method of the invention in combination with
CC dipteropod triepoxides to kill tumours by inducing apoptosis.
XX
XX
SQ Sequence 455 AA;
Query Match 100.0%; Score 2487; DB 23; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.6e-181;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLPLVLELLVGIYPSGVILVPHLGDREKRDVCPGKGIYHPQNNISICT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVILVPHLGDREKRDVCPGKGIYHPQNNISICT 60
QY 61 KCHKGTYLYNDPCPGQDTCRECESGSFTASENHLRHLCSCSKCKEKGVEISSCTVD 120
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Db 121 RDVCGCRKNQRYHYWSENLFQCFNCGLNGTVHLSCQEKONTVCTCHAGFLRENECV 180
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 Db 241 SKLSTVCGSTPEKKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSSTSTYT 300
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 Db 301 PGDCPNFAAPRREYAPYOGADPILATALASDPINPLQKWEBSAHKPOSIDTDDPATLY 360
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 Db 361 AVVENPPLRWKKEFVRRLGSDHEIDRLDLONGRCLEAQSMLATWRRTPRREATLEL 420
 QY 421 LGRVLRMDLIGCLEDEIEBALCGPALPPAPSLLR 455
 Db 421 LGRVLRMDLIGCLEDEIEBALCGPALPPAPSLLR 455

RESULT 15

AA11082
 ID AA11082 standard; Protein; 455 AA.
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 AC AA11082;
 XX
 DT 24-MAY-1991 (first entry)
 XX
 DE Human 55kD TNF-binding protein.
 XX
 KM Tumour Necrosis Factor; binding proteins; septic shock;
 KW auto-immune glomerulonephritis; lymphokine; cytokine.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 54
 FT Modified-site 145 /label= putative N-glycosylation site
 FT Modified-site 151 /label= putative N-glycosylation site
 FT Modified-site 270 /label= putative N-glycosylation site
 FT Region 212..230 /label= putative N-glycosylation site
 FT Peptide 1..28 /label= transmembrane region
 FT Peptide /label= signal peptide
 XX
 PN EP417563-A.
 PD 20-MAR-1991.
 XX
 PF 31-AUG-1990; 90EP-0116707.
 XX
 PR 20-APR-1990; 90CH-0001347.
 PR 12-SEP-1989; 89CH-0003319.
 PR 08-MAR-1990; 90CH-0000746.
 XX
 PA (HOF) HOFFMANN-LA ROCHE AG.
 XX
 PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
 PI Schlaeger EJ;
 XX
 DR WPI: 1991-081851/12.
 DR N-PSDB; AAO10955.
 XX
 PT Insoluble tumour necrosis factor binding proteins - and DNA
 PT encoding them, useful in pharmaceutical prods. and for antibody
 PT prodn.
 XX

PS Claim 1; Fig 1; 26pp; German.
 XX
 CC Partial amino acid sequences were determined for the 55 and 75kD
 CC TNF-BPs (see AA11072-R11081) and oligonucleotide primers were
 CC synthesised based on these partial sequences. The primers were used
 CC to produce a cDNA fragment for use as a probe to screen a human
 CC placental cDNA bank constructed in lambda gt11. Positive clones were
 CC identified and sequenced. DNA constructs comprising the TNF-BP coding
 CC sequence may also contain a fragment encoding a human Ig domain.
 CC Recombinant constructs are used to transform cells to confer
 CC improved TNF-binding properties.
 CC See also AAO10956.
 CC
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 SQ Sequence 455 AA;

Query Match 99.9%; Score 2484; DB 12; Length 455;
 Best Local Similarity 99.8%; Pred. No. 7,7e-181;
 Matches 454; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 KCHKGTLYNDCCPGGDDTCRECESSFTASENHLRHCISCKRKEKMGVEISSCTVD 120
 Db 61 KCHKGTLYNDCCPGGDDTCRECESSFTASENHLRHCISCKRKEKMGVEISSCTVD 120
 QY 121 RDVCGCRKNQRYHYWSENLFQCFNCGLNGTVHLSCQEKONTVCTCHAGFLRENECV 180
 Db 121 RDVCGCRKNQRYHYWSENLFQCFNCGLNGTVHLSCQEKONTVCTCHAGFLRENECV 180
 QY 181 SCSNCKKSLBCTKLCLEPOIENVKGTEDSGTTLPLVIFFGCLLSLFLGLMYRYORWK 240
 Db 181 SCSNCKKSLBCTKLCLEPOIENVKGTEDSGTTLPLVIFFGCLLSLFLGLMYRYORWK 240
 QY 241 SKLSTVCGSTPEKKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSSTSTYT 300
 Db 241 SKLSTVCGSTPEKKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSSTSTYT 300
 QY 301 PGDCPNFAAPRREYAPYOGADPILATALASDPINPLQKWEBSAHKPOSIDTDDPATLY 360
 Db 301 PGDCPNFAAPRREYAPYOGADPILATALASDPINPLQKWEBSAHKPOSIDTDDPATLY 360
 QY 361 AVVENPPLRWKKEFVRRLGSDHEIDRLDLONGRCLEAQSMLATWRRTPRREATLEL 420
 Db 361 AVVENPPLRWKKEFVRRLGSDHEIDRLDLONGRCLEAQSMLATWRRTPRREATLEL 420
 QY 421 LGRVLRMDLIGCLEDEIEBALCGPALPPAPSLLR 455
 Db 421 LGRVLRMDLIGCLEDEIEBALCGPALPPAPSLLR 455

Search completed: December 27, 2002, 15:07:50
 Job time : 42 secs

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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:08:44 ; Search time 12 Seconds

(without alignments)
656,494 Million cell updates/sec

Title: US-09-899-429a-2

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Gapop 10.0 , Gapext 0.5

Searched: 109717 seqs, 17314136 residues

Total number of hits satisfying chosen parameters: 109717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2487	100.0	455 9 US-09-898-234-2	Sequence 2, Appl1
2	2487	100.0	455 9 US-09-898-234-17	Sequence 17, Appl1
3	2487	100.0	455 9 US-09-756-854-5	Sequence 5, Appl1
4	2487	100.0	455 9 US-09-899-429a-2	Sequence 2, Appl1
5	2487	100.0	455 9 US-09-899-429a-27	Sequence 27, Appl1
6	2487	100.0	455 9 US-10-041-574-5	Sequence 5, Appl1
7	2487	100.0	455 9 US-09-792-356-2	Sequence 2, Appl1
8	2487	100.0	455 9 US-09-792-356-17	Sequence 17, Appl1
9	2487	100.0	455 10 US-09-826-212-3	Sequence 3, Appl1
10	2487	100.0	455 10 US-09-333-966-5	Sequence 5, Appl1
11	2487	100.0	455 10 US-09-027-287-3	Sequence 3, Appl1
12	2487	100.0	455 10 US-09-874-138-3	Sequence 3, Appl1
13	2487	100.0	455 10 US-09-840-707a-16	Sequence 16, Appl1
14	2487	100.0	455 10 US-09-252-6568-3	Sequence 3, Appl1
15	2487	100.0	455 10 US-09-899-422-2	Sequence 2, Appl1
16	2487	100.0	455 10 US-09-899-422-17	Sequence 17, Appl1
17	2487	100.0	455 10 US-09-935-727-5	Sequence 5, Appl1
18	2487	100.0	455 12 US-10-005-843-3	Sequence 3, Appl1
19	2487	100.0	455 12 US-10-120-397-2	Sequence 2, Appl1

20	2053	82.5	371 9 US-09-898-234-12	Sequence 12, Appl1
21	2053	82.5	371 9 US-09-792-356-12	Sequence 12, Appl1
22	2053	82.5	371 10 US-09-899-422-12	Sequence 12, Appl1
23	2039	82.0	371 9 US-09-899-429a-22	Sequence 22, Appl1
24	1550.5	62.3	461 9 US-09-898-234-15	Sequence 15, Appl1
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27	1550.5	62.3	461 10 US-09-899-422-15	Sequence 15, Appl1
28	1517	61.0	471 10 US-09-970-532-2	Sequence 2, Appl1
29	1194	48.0	213 9 US-10-125-062-1	Sequence 1, Appl1
30	1192	47.9	211 9 US-09-899-429a-8	Sequence 8, Appl1
31	1141	45.9	201 9 US-09-899-429a-14	Sequence 14, Appl1
32	1121	45.1	197 9 US-10-112-793-21	Sequence 21, Appl1
33	1117.5	44.9	200 9 US-09-899-429a-12	Sequence 12, Appl1
34	1066.5	42.9	190 9 US-09-899-429a-18	Sequence 18, Appl1
35	1051	42.3	183 9 US-09-899-429a-10	Sequence 10, Appl1
36	1005.5	40.4	336 10 US-09-756-186-8	Sequence 8, Appl1
37	1000	40.2	173 9 US-09-899-429a-16	Sequence 16, Appl1
38	992	39.9	172 9 US-09-899-429a-20	Sequence 20, Appl1
39	979	39.4	285 10 US-09-756-186-6	Sequence 6, Appl1
40	941	37.8	161 9 US-09-898-234-4	Sequence 4, Appl1
41	941	37.8	161 9 US-09-899-429a-4	Sequence 4, Appl1
42	941	37.8	161 9 US-09-792-356-4	Sequence 4, Appl1
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44	941	37.8	161 10 US-09-907-263-2	Sequence 2, Appl1
45	941	37.8	162 9 US-09-899-429a-6	Sequence 6, Appl1

ALIGNMENTS

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RESULT 1
US-09-898-234-2
; Sequence 2, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Seretova, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: rhnm
; FILE REFERENCE: 98/385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-898-234-2
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Best Local Similarity 100.0%; Pred. No. 4, 9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIIGLVPHLGDRKRDVCPQGRYTHPNNSICCT 60
OY 61 KCHNGTLYVNDGPGPGDTGCRRECSGSPFASEHNLHRCISGCKREKMGVEISSCTVD 120
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Db      121 RDTVCGCRNNQYRHWSENLFOCFNCSLCNGTVHLSCEKONTVCTCHAGFELRENECV 180
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RESULT 2
US-09-898-234-17
; Sequence 17, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding proteins and DNAs Coding for
; TITLE OF INVENTION: them
; FILE REFERENCE: 98,385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: TNF-R2
US-09-898-234-17

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Query Match      100.0%; Score 2487; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MGLSTVPDLPLPLVLELVGTPSGVIGVPHLDREKRDVCPQKRYIHQNNISICT 60
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Db      361 AVEENVPLRMKEFVRRLGSDHEIDRLQNGRCLEAQSMLATWRRRTPRRATLEL 420
QY      421 LGRVLRMDLGLCLEDIEFALCPAALPPAPSLR 455
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RESULT 3
US-09-756-854-5
; Sequence 5, Application US/09756854
; Patent No. US20020164684A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Fan, Ping
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor Tr3
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-756-854-5

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Query Match 100.0%; Score 2487; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELVLGYIPSGVIGLVPHLGDREKRDSCVPOGKYIHPONNISCTT 60
DB 1 MGLSTVPDLLPLVLELVLGYIPSGVIGLVPHLGDREKRDSCVPOGKYIHPONNISCTT 60
QY 61 KCHKGTLYLNDCCPGPDOTDCRECESSGFTASBNHLRHCLSCSKREKEMQVEISSCTVD 120
DB 61 KCHKGTLYLNDCCPGPDOTDCRECESSGFTASBNHLRHCLSCSKREKEMQVEISSCTVD 120
QY 121 RDVYCGCRKQRYHYMSSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
DB 121 RDVYCGCRKQRYHYMSSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
QY 181 SCGNCKSLSECTKCLPQIENVKGTEDSGTTLPLVIFFGCLLSLFLIGLWRYORWK 240
DB 181 SCGNCKSLSECTKCLPQIENVKGTEDSGTTLPLVIFFGCLLSLFLIGLWRYORWK 240
QY 241 SKLYSIYCGKSTPEKEBELGTTTKPLAPNPSFSPGFTPLGFSFVPSSTFTSSSTYT 300
DB 241 SKLYSIYCGKSTPEKEBELGTTTKPLAPNPSFSPGFTPLGFSFVPSSTFTSSSTYT 300
QY 301 PGDCPNPAARRREVAPPYOGADPLATALASDPIPNPLOKWEBSAHKPOSLDDDDPATLY 360
DB 301 PGDCPNPAARRREVAPPYOGADPLATALASDPIPNPLOKWEBSAHKPOSLDDDDPATLY 360
QY 361 AVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPREATLEL 420
DB 361 AVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDLLGLCLEIDIEELCGPALPPAPSLLR 455
DB 421 LGRVLRMDLLGLCLEIDIEELCGPALPPAPSLLR 455

RESULT 4
US-09-899-429a-2
; Sequence 27, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hummel, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-1
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-899-429a-2

Query Match 100.0%; Score 2487; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELVLGYIPSGVIGLVPHLGDREKRDSCVPOGKYIHPONNISCTT 60
DB 1 MGLSTVPDLLPLVLELVLGYIPSGVIGLVPHLGDREKRDSCVPOGKYIHPONNISCTT 60
QY 61 KCHKGTLYLNDCCPGPDOTDCRECESSGFTASBNHLRHCLSCSKREKEMQVEISSCTVD 120
DB 61 KCHKGTLYLNDCCPGPDOTDCRECESSGFTASBNHLRHCLSCSKREKEMQVEISSCTVD 120
QY 121 RDVYCGCRKQRYHYMSSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
DB 121 RDVYCGCRKQRYHYMSSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
QY 181 SCGNCKSLSECTKCLPQIENVKGTEDSGTTLPLVIFFGCLLSLFLIGLWRYORWK 240
DB 181 SCGNCKSLSECTKCLPQIENVKGTEDSGTTLPLVIFFGCLLSLFLIGLWRYORWK 240
QY 241 SKLYSIYCGKSTPEKEBELGTTTKPLAPNPSFSPGFTPLGFSFVPSSTFTSSSTYT 300
DB 241 SKLYSIYCGKSTPEKEBELGTTTKPLAPNPSFSPGFTPLGFSFVPSSTFTSSSTYT 300
QY 301 PGDCPNPAARRREVAPPYOGADPLATALASDPIPNPLOKWEBSAHKPOSLDDDDPATLY 360
DB 301 PGDCPNPAARRREVAPPYOGADPLATALASDPIPNPLOKWEBSAHKPOSLDDDDPATLY 360
QY 361 AVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPREATLEL 420
DB 361 AVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDLLGLCLEIDIEELCGPALPPAPSLLR 455
DB 421 LGRVLRMDLLGLCLEIDIEELCGPALPPAPSLLR 455

RESULT 5
US-09-899-429a-27
; Sequence 27, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hummel, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-1
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R 1n
US-09-899-429a-27

Query Match 100.0%; Score 2487; DB 9; Length 455;

Best Local Similarity 100.0%; Pred. NO. 4.9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGLSTVPDLLLPLVLLLELWVGYSSGVIYGVPHLGDKEKRDVSCPOGKYTHPONNSICT	60
Dp	1	MGLSTVPDLLLPLVLLLELWVGYSSGVIYGVPHLGDKEKRDVSCPOGKYTHPONNSICT	60
Qy	61	KCHGKGYTYLNDCCPGPGDDTCRECESSGFTASENHLHCLSCSKCKREMOVEISSCTVD	120
Dp	61	KCHGKGYTYLNDCCPGPGDDTCRECESSGFTASENHLHCLSCSKCKREMOVEISSCTVD	120
Qy	121	RDYVCGCGKKNQYRHAYWSENLPQCNGSLCNGTVHLSGCKOMTVYCHAGFFLRENECV	180
Dp	121	RDYVCGCGKKNQYRHAYWSENLPQCNGSLCNGTVHLSGCKOMTVYCHAGFFLRENECV	180
Qy	181	SCSNCKRSLECTKLCLPQIENWVKTEDSGTVLLPLVIFGGLCLSLPIGLWRYORWK	240
Dp	181	SCSNCKRSLECTKLCLPQIENWVKTEDSGTVLLPLVIFGGLCLSLPIGLWRYORWK	240
Qy	241	SKLTSIYCGKSTPEKBEELBETTTKPLAPNPSPSPPTGFTPLGFSVPBSTSSSTYT	300
Dp	241	SKLTSIYCGKSTPEKBEELBETTTKPLAPNPSPSPPTGFTPLGFSVPBSTSSSTYT	300
Qy	301	PGDCPNFAAPRREVAAPYOGADPLIATALASDPILPNLQKMEBSAHKPOSLDIDDDPATLY	360
Dp	301	PGDCPNFAAPRREVAAPYOGADPLIATALASDPILPNLQKMEBSAHKPOSLDIDDDPATLY	360
Qy	361	AVVENVPPLRMKEVVRRLGLSDHEIDRLFLQNGRCLEAOYSMLATVRRRTTPREAREL	420
Dp	361	AVVENVPPLRMKEVVRRLGLSDHEIDRLFLQNGRCLEAOYSMLATVRRRTTPREAREL	420
Qy	421	LGRVLRDMDDLGCLEDEIEEALCGFAALPPAPSLLR	455
Dp	421	LGRVLRDMDDLGCLEDEIEEALCGFAALPPAPSLLR	455

```

RESULT 6
US-10-041-574-5
; Sequence 5, Application US/10041574
; Patent No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/521,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1996-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-041-574-5

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Query Match	100.0%	Score 2487	DB 9	Length 455
Best Local Similarity	100.0%	Pred. No. 4,9e-158		
Matches 455	Conservative 0	Mismatches 0	Indels 0	Gaps 0
1	MGLSTVPDLLPIVLELTVGIPSGVIGLVPHLDREKRSDVCPQGXIIHPQNNISICT	60		

Db	1	MGLSTVPDLLPLPLVLELLELVGIVPYSVIGLVPHLHGDREKRDVSPQSKYIHPNNNSLCTT	60
QY	61	KCHKGYLYLNDCKPBPQGDPTDCCRECESSFPASENHLRHCLSCSKCRKEMGOVEISSCTVD	120
Db	61	KCHKGYLYLNDCKPBPQGDPTDCCRECESSFPASENHLRHCLSCSKCRKEMGOVEISSCTVD	120
QY	121	RDYVCGCRKNQYRHYWSEBNLPQCFNCSLCLNGVYHLSOQEKONTVCTCHAGFLRENECV	180
Db	121	RDYVCGCRKNQYRHYWSEBNLPQCFNCSLCLNGVYHLSOQEKONTVCTCHAGFLRENECV	180
QY	181	SCSNCKSKSEBTKLCLPQIENKVTEDBSGTTVLLPLVIFFGCLLSLPLGLMRYRQRMK	240
Db	181	SCSNCKSKSEBTKLCLPQIENKVTEDBSGTTVLLPLVIFFGCLLSLPLGLMRYRQRMK	240
QY	241	SKLYSIYCGKSTPEKEBELBGTTHKPLAPNPSPPPTGFTPLTGFSVPBSSTTSSSYTT	300
Db	241	SKLYSIYCGKSTPEKEBELBGTTHKPLAPNPSPPPTGFTPLTGFSVPBSSTTSSSYTT	300
QY	301	PGDCPNFAAPREVAAPYOGADPLATATASDPLPNLQKWEBSAHKPOSLDDDDPATLY	360
Db	301	PGDCPNFAAPREVAAPYOGADPLATATASDPLPNLQKWEBSAHKPOSLDDDDPATLY	360
QY	361	AVVENVPPLRKKEVVRRLGSDHEIDRLQLONGRCULREAOYSMLATMRRRTPRREATLEL	420
Db	361	AVVENVPPLRKKEVVRRLGSDHEIDRLQLONGRCULREAOYSMLATMRRRTPRREATLEL	420
QY	421	LGRVLRDMDLGCLLEDEEALCGPAALPPAPSLLR	455
Db	421	LGRVLRDMDLGCLLEDEEALCGPAALPPAPSLLR	455

```

RESULT 7
US-09-792-356-2
; Sequence 2, Application US/09792356
; Publication NO. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hammler, Adolph
; APPLICANT: Maurer-Pogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE OF INVENTION: Them
; FILE REFERENCE: 98, 385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-792-356-2

```

Query Match	100.0%	Score 2487	DB 9	Length 455
Best Local Similarity	100.0%	Pred. No. 4.9e-158		
Matches 455	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MGSTVDPDLLPEVLLELVGTPSGVIGLVPHLDRKRDKRSVCPQGYIHPQNNISICT	60	
Db	1	MGSTVDPDLLPEVLLELVGTPSGVIGLVPHLDRKRDKRSVCPQGYIHPQNNISICT	60	
QY	61	KCHKGTYLNDCCPGGDDTCRECEBSGFTASENHLRHLCSCKRKEMGOYEISSCTVD	120	

Db 61 KCHKGYLVNDGPGDPTDCRECESSFTASENHLRHCLSCSKREKMGVEISSCTVD 120
QY 121 RDVYCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
Db 121 RDVYCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
QY 181 SCGNCKKSLCCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
Db 181 SCGNCKKSLCCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
QY 241 SKLYSIYCGSKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
Db 241 SKLYSIYCGSKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
QY 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPLOWEDSAHKPQSLDTPDPTLY 360
Db 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPLOWEDSAHKPQSLDTPDPTLY 360
QY 361 AVVENNPRLMKKEFVRRLGSDHEIDRLQNGRCLEADYSMLATWRRRTPREATLEL 420
Db 361 AVVENNPRLMKKEFVRRLGSDHEIDRLQNGRCLEADYSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDLGLCLEDIEEALCGPALPAPSLR 455
Db 421 LGRVLRMDLGLCLEDIEEALCGPALPAPSLR 455

RESULT 8

US-09-792-356-17
; Sequence 17, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hammler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stracova, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE OF INVENTION: Them
; FILE REFERENCE: 98,385-6
; CURRENT APPLICATION NUMBER: US/09/792,356
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R 1n
; OTHER INFORMATION: LTNF-R2
US-09-792-356-17

Query Match 100.0%; Score 2487; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSTVPDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVCPQCKYIHPONNISICT 60
Db 1 MGSTVPDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVCPQCKYIHPONNISICT 60
QY 61 KCHKGYLVNDGPGDPTDCRECESSFTASENHLRHCLSCSKREKMGVEISSCTVD 120
Db 61 KCHKGYLVNDGPGDPTDCRECESSFTASENHLRHCLSCSKREKMGVEISSCTVD 120

QY 121 RDVYCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
Db 121 RDVYCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
QY 181 SCGNCKKSLCCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
Db 181 SCGNCKKSLCCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
QY 241 SKLYSIYCGSKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
Db 241 SKLYSIYCGSKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
QY 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPLOWEDSAHKPQSLDTPDPTLY 360
Db 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPLOWEDSAHKPQSLDTPDPTLY 360
QY 361 AVVENNPRLMKKEFVRRLGSDHEIDRLQNGRCLEADYSMLATWRRRTPREATLEL 420
Db 361 AVVENNPRLMKKEFVRRLGSDHEIDRLQNGRCLEADYSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDLGLCLEDIEEALCGPALPAPSLR 455
Db 421 LGRVLRMDLGLCLEDIEEALCGPALPAPSLR 455

RESULT 9

US-09-826-212-3
; Sequence 3, Application US/09826212
; Patent No. US20010021516A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488,1280006
; CURRENT APPLICATION NUMBER: US/09/826,212
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-212-3

Query Match 100.0%; Score 2487; DB 10; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSTVPDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVCPQCKYIHPONNISICT 60
Db 1 MGSTVPDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVCPQCKYIHPONNISICT 60
QY 61 KCHKGYLVNDGPGDPTDCRECESSFTASENHLRHCLSCSKREKMGVEISSCTVD 120
Db 61 KCHKGYLVNDGPGDPTDCRECESSFTASENHLRHCLSCSKREKMGVEISSCTVD 120
QY 121 RDVYCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
Db 121 RDVYCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
QY 181 SCGNCKKSLCCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
Db 181 SCGNCKKSLCCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
QY 241 SKLYSIYCGSKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
Db 241 SKLYSIYCGSKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
QY 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPLOWEDSAHKPQSLDTPDPTLY 360
Db 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPLOWEDSAHKPQSLDTPDPTLY 360

Db 301 PGDCPFAAPRRREVAAPYOGADPILATASDPINPDLQKWDSSAHKPOSLOTDDPATLY 360

QY 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQLONGRCILREAOYSMLATWRRTPRREATTLEL 420

Db 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQLONGRCILREAOYSMLATWRRTPRREATTLEL 420

QY 421 LGRVLRMDMLGLCLDIEEALCGPALPPAPSLLR 455

Db 421 LGRVLRMDMLGLCLDIEEALCGPALPPAPSLLR 455

RESULT 10

US-09-333-966-5

; Sequence 5, Application US/09333966

; Patent No. US2002009773A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ni, Jian

; APPLICANT: Dixit, Vishva

; APPLICANT: Gentz, Reiner L.

; APPLICANT: Dillon, Patrick J.

; TITLE OF INVENTION: Death Domain Containing Receptors

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

; STREET: 1100 New York Ave., NW, Suite 600

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/333,966

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/815,469

; FILING DATE:

; APPLICATION NUMBER: No. US2002009773A1 yet Assigned

; FILING DATE: 06-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/028,711

; FILING DATE: 17-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/013,285

; FILING DATE: 12-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Steffe, Eric K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488, 0310003/EKS/KRM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 455 amino acids

; TYPE: amino acid

; STRANDEDNESS: NO. US2002009773A1 Relevant

; TOPOLOGY: No. US2002009773A1 Relevant

; MOLECULE TYPE: protein

US-09-333-966-5

Query Match 100.0%; Score 2487; DB 10; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.9e-158;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVYLLELVGTPSGVIGLVPHLGDREKRSVCPQGYIHPONNSICT 60

Db 1 MGLSTVPDLLPLVYLLELVGTPSGVIGLVPHLGDREKRSVCPQGYIHPONNSICT 60

QY 61 KCHKGTLYLNDGPGQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGVEISSCTVD 120

Db 61 KCHKGTLYLNDGPGQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGVEISSCTVD 120

QY 121 RDTVCGCKRNQYRHWSENLFOCFNCSLCLNGTVHLSCEBKQNTVCTGAGFFLRNECV 180

Db 121 RDTVCGCKRNQYRHWSENLFOCFNCSLCLNGTVHLSCEBKQNTVCTGAGFFLRNECV 180

QY 181 SCSNCKRSLECKTKLCPQIENYKGTEDSGTVLPLVIFFGCLLSLPLIGLMTYRQRK 240

Db 181 SCSNCKRSLECKTKLCPQIENYKGTEDSGTVLPLVIFFGCLLSLPLIGLMTYRQRK 240

QY 241 SKLYSTVCGSKTPKEKGELEGTTTKPLADNPSPPTPGFTPLGFSVPVSSFTSSSTYT 300

Db 241 SKLYSTVCGSKTPKEKGELEGTTTKPLADNPSPPTPGFTPLGFSVPVSSFTSSSTYT 300

QY 301 PGDCPFAAPRRREVAAPYOGADPILATASDPINPDLQKWDSSAHKPOSLOTDDPATLY 360

Db 301 PGDCPFAAPRRREVAAPYOGADPILATASDPINPDLQKWDSSAHKPOSLOTDDPATLY 360

QY 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQLONGRCILREAOYSMLATWRRTPRREATTLEL 420

Db 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQLONGRCILREAOYSMLATWRRTPRREATTLEL 420

QY 421 LGRVLRMDMLGLCLDIEEALCGPALPPAPSLLR 455

Db 421 LGRVLRMDMLGLCLDIEEALCGPALPPAPSLLR 455

RESULT 11

US-09-027-287-3

; Sequence 3, Application US/09027287A

; Patent No. US20020064869A1

; GENERAL INFORMATION:

; APPLICANT: Ebner, Reinhard

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ruben, Steven M.

; APPLICANT: Dillrich, Stephen

; TITLE OF INVENTION: Apoptosis Inducing Molecule II

; FILE REFERENCE: 1488, 0650004

; CURRENT APPLICATION NUMBER: US/09/027,287A

; EARLIER FILING DATE: 1998-02-20

; EARLIER APPLICATION NUMBER: US 09/003,886

; EARLIER FILING DATE: 1998-01-07

; EARLIER APPLICATION NUMBER: US 08/822,953

; EARLIER FILING DATE: 1997-03-21

; EARLIER APPLICATION NUMBER: US 60/030,157

; EARLIER FILING DATE: 1996-10-31

; EARLIER APPLICATION NUMBER: US 60/013,923

; EARLIER FILING DATE: 1996-03-22

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 3

; LENGTH: 455

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-027-287-3

Query Match 100.0%; Score 2487; DB 10; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.9e-158;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVYLLELVGTPSGVIGLVPHLGDREKRSVCPQGYIHPONNSICT 60

Db 1 MGLSTVPDLLPLVYLLELVGTPSGVIGLVPHLGDREKRSVCPQGYIHPONNSICT 60

QY 61 KCHKGTLYLNDGPGQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGVEISSCTVD 120

Db 61 KCHKGTLYLNDGPGQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGVEISSCTVD 120

QY 121 RDTVCGCKRNQYRHWSENLFOCFNCSLCLNGTVHLSCEBKQNTVCTGAGFFLRNECV 180

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Db 121 RDTVCCGRKNOYRHVYSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
OY 181 SCGNCKRSLECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORMK 240
Db 181 SCGNCKRSLECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORMK 240
OY 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTPLGFSVPVSSSTSTYT 300
Db 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTPLGFSVPVSSSTSTYT 300
OY 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPQKWEDESAHKPOSLODDPATLY 360
Db 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPQKWEDESAHKPOSLODDPATLY 360
OY 361 AVVENYPLRMKEFVRRLGSDHEIDRLDELONRCRLREAOYSMLATWRRTPPREATLEL 420
Db 361 AVVENYPLRMKEFVRRLGSDHEIDRLDELONRCRLREAOYSMLATWRRTPPREATLEL 420
OY 421 LGRVLDMDLGLCLEDIEEALCGPALPPAPSLLR 455
Db 421 LGRVLDMDLGLCLEDIEEALCGPALPPAPSLLR 455

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RESULT 12

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US-09-874-138-3
; Sequence 3, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.1310006
; CURRENT APPLICATION NUMBER: US/09/874,138
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565,009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-138-3

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Query Match 100.0%; Score 2487; DB 10: Length 455;

Best Local Similarity 100.0%; Pred. No. 4,9e-158;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGRDKRDSVCPQGYTHPONNSICT 60
OY 61 KCHKGTLYLVNDGCPGPDGDTDCRCESGSPFASBNHLRHCLSCSKCKREMOVEISSCTVD 120
Db 61 KCHKGTLYLVNDGCPGPDGDTDCRCESGSPFASBNHLRHCLSCSKCKREMOVEISSCTVD 120
OY 121 RDTVCCGRKNOYRHVYSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
Db 121 RDTVCCGRKNOYRHVYSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180

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OY 181 SCGNCKRSLECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORMK 240
Db 181 SCGNCKRSLECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORMK 240
OY 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTPLGFSVPVSSSTSTYT 300
Db 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTPLGFSVPVSSSTSTYT 300
OY 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPQKWEDESAHKPOSLODDPATLY 360
Db 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPQKWEDESAHKPOSLODDPATLY 360
OY 361 AVVENYPLRMKEFVRRLGSDHEIDRLDELONRCRLREAOYSMLATWRRTPPREATLEL 420
Db 361 AVVENYPLRMKEFVRRLGSDHEIDRLDELONRCRLREAOYSMLATWRRTPPREATLEL 420
OY 421 LGRVLDMDLGLCLEDIEEALCGPALPPAPSLLR 455
Db 421 LGRVLDMDLGLCLEDIEEALCGPALPPAPSLLR 455

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RESULT 13

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US-09-840-707A-16
; Sequence 16, Application US/09840707A
; Patent No. US2002007276A1
; GENERAL INFORMATION:
; APPLICANT: Fredelg, Terry M.
; APPLICANT: Ignatiev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840,707A
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Tumor Necrosis Factor p55 Receptor
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAA36753/GenBank
; DATABASE ENTRY DATE: 1995-08-03
US-09-840-707A-16

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Query Match 100.0%; Score 2487; DB 10: Length 455;

Best Local Similarity 100.0%; Pred. No. 4,9e-158;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGRDKRDSVCPQGYTHPONNSICT 60
Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGRDKRDSVCPQGYTHPONNSICT 60
OY 61 KCHKGTLYLVNDGCPGPDGDTDCRCESGSPFASBNHLRHCLSCSKCKREMOVEISSCTVD 120
Db 61 KCHKGTLYLVNDGCPGPDGDTDCRCESGSPFASBNHLRHCLSCSKCKREMOVEISSCTVD 120
OY 121 RDTVCCGRKNOYRHVYSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
Db 121 RDTVCCGRKNOYRHVYSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRENECV 180
OY 181 SCGNCKRSLECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORMK 240
Db 181 SCGNCKRSLECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORMK 240
OY 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTPLGFSVPVSSSTSTYT 300
Db 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTPLGFSVPVSSSTSTYT 300

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Db 241 SKLVSIVCGKSTPEKEGLEGTGTTKPLAPNPSFSPPTGFTPLGFSVPVSSFTSSSTYT 300
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Db 301 PGDCNFAPARRREVAAPYOGADPILATALASDPINPLOCKWEDSAHKPOSLDTPDPAATLY 360
Qy 361 AVENVPPLRKMEFVRRLGSLDHEIDRLLELONGRCLREAOYSMLATWRRRTTREATLEL 420
Db 361 AVENVPPLRKMEFVRRLGSLDHEIDRLLELONGRCLREAOYSMLATWRRRTTREATLEL 420
Qy 421 IGRVLDMDLGCLDIEEALCGPALPAPSLR 455
Db 421 IGRVLDMDLGCLDIEEALCGPALPAPSLR 455

RESULT 14
US-09-252-656B-3
; Sequence 3, Application US/09252656B
; Patent No. US20020081647A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Zhang, Jun
; APPLICANT: Ullrich, Stephen
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.0650006
; CURRENT FILING DATE: US/09/252.656B
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/075,409
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/027,287
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/003,886
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 08/822,953
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/013,923
; PRIOR FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: US 60/030,157
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-656B-3

Query Match 100.0%; Score 2487; DB 10; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 KCHKGTYLYNDCPGGQOTDRCESGSGFTASENHLRHCLSCSKCRKMGVEIISCTVD 120
Qy 121 RDYVCGCKKNQYRHWSENLFQCFNCSICLNGTYHLSQOEKONTVCCTHAGFTLRENECV 180
Db 121 RDYVCGCKKNQYRHWSENLFQCFNCSICLNGTYHLSQOEKONTVCCTHAGFTLRENECV 180
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Db 181 SC5NCKKSLCTKICLPQIENVKGTEGDSGTVLLPLVIFGCLLSLFIQLMRYORWK 240
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Db 241 SKLVSIVCGKSTPEKEGLEGTGTTKPLAPNPSFSPPTGFTPLGFSVPVSSFTSSSTYT 300

Qy 301 PGDCNFAPARRREVAAPYOGADPILATALASDPINPLOCKWEDSAHKPOSLDTPDPAATLY 360
Db 301 PGDCNFAPARRREVAAPYOGADPILATALASDPINPLOCKWEDSAHKPOSLDTPDPAATLY 360
Qy 361 AVENVPPLRKMEFVRRLGSLDHEIDRLLELONGRCLREAOYSMLATWRRRTTREATLEL 420
Db 361 AVENVPPLRKMEFVRRLGSLDHEIDRLLELONGRCLREAOYSMLATWRRRTTREATLEL 420
Qy 421 IGRVLDMDLGCLDIEEALCGPALPAPSLR 455
Db 421 IGRVLDMDLGCLDIEEALCGPALPAPSLR 455

RESULT 15
US-09-899-422-2
; Sequence 2, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98.385-H
; CURRENT FILING DATE: US/09/899.422
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-899-422-2

Query Match 100.0%; Score 2487; DB 10; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGLSTVPDLLPLVLLLELVGIYPSGVIGLVPHLGDRKRDVSCPGKYIHPONNISICT 60
Qy 61 KCHKGTYLYNDCPGGQOTDRCESGSGFTASENHLRHCLSCSKCRKMGVEIISCTVD 120
Db 61 KCHKGTYLYNDCPGGQOTDRCESGSGFTASENHLRHCLSCSKCRKMGVEIISCTVD 120
Qy 121 RDYVCGCKKNQYRHWSENLFQCFNCSICLNGTYHLSQOEKONTVCCTHAGFTLRENECV 180
Db 121 RDYVCGCKKNQYRHWSENLFQCFNCSICLNGTYHLSQOEKONTVCCTHAGFTLRENECV 180
Qy 181 SC5NCKKSLCTKICLPQIENVKGTEGDSGTVLLPLVIFGCLLSLFIQLMRYORWK 240
Db 181 SC5NCKKSLCTKICLPQIENVKGTEGDSGTVLLPLVIFGCLLSLFIQLMRYORWK 240
Qy 241 SKLVSIVCGKSTPEKEGLEGTGTTKPLAPNPSFSPPTGFTPLGFSVPVSSFTSSSTYT 300
Db 241 SKLVSIVCGKSTPEKEGLEGTGTTKPLAPNPSFSPPTGFTPLGFSVPVSSFTSSSTYT 300
Qy 301 PGDCNFAPARRREVAAPYOGADPILATALASDPINPLOCKWEDSAHKPOSLDTPDPAATLY 360
Db 301 PGDCNFAPARRREVAAPYOGADPILATALASDPINPLOCKWEDSAHKPOSLDTPDPAATLY 360

Qy 361 AVVENPPLWKEFVRRLGSDHEIDRLQLONGRCLREAOYSMLATWRRRTPREATLEL 420
|||
Db 361 AVVENPPLWKEFVRRLGSDHEIDRLQLONGRCLREAOYSMLATWRRRTPREATLEL 420
|||
Qy 421 LGRVLRDMDLGGCLDEIEEALCGPALPPAPSLR 455
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Db 421 LGRVLRDMDLGGCLDEIEEALCGPALPPAPSLR 455
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Search completed: December 27, 2002, 15:13:02
Job time : 13 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2002, 15:07:00 ; Search time 17 Seconds

(without alignments)
787,496 Million cell updates/sec

Title: US-09-899-429a-2

Perfect score: 2487
Sequence: 1 MGUSTVDPDLLPLVLELLV.....DIEALCPALPPAPSLR 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2487	100.0	455	1	US-08-837-941-2
3	2487	100.0	455	2	US-08-126-016-2
4	2487	100.0	455	4	US-08-815-469-5
5	2487	100.0	455	4	US-09-006-353a-3
6	2487	100.0	455	4	US-09-527-236a-5
7	2487	100.0	455	4	US-08-054-970-2
8	2487	100.0	455	4	US-09-565-918-4
9	2487	100.0	455	4	US-09-573-986-3
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13	2463.5	99.1	909	4	US-09-448-868-4
14	2457	98.8	453	4	US-09-086-483a-5
15	1558	62.6	280	3	US-08-974-022-46
16	1558	62.6	280	4	US-08-795-445a-46
17	1558	62.6	280	4	US-08-795-447a-46
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19	1558	62.6	280	4	US-08-795-446b-46
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21	1517	61.0	471	4	US-09-513-007-2
22	1124	45.2	139	1	US-08-050-319b-48
23	1124	45.1	199	2	US-08-465-982-48
24	1121	45.1	197	4	US-08-828-683a-21
25	1005.5	40.4	336	4	US-08-804-166-8
26	1005.5	40.4	336	4	US-08-910-991-8
27	979	39.4	285	4	US-08-804-166-6

28	979	39.4	285	4	US-08-910-991-6	Sequence 6, App11
29	946	38.0	167	1	US-08-050-319b-2	Sequence 2, App11
30	946	38.0	167	1	US-08-050-319b-57	Sequence 57, App1
31	946	38.0	167	2	US-08-465-982-2	Sequence 2, App1
32	946	38.0	167	2	US-08-465-982-57	Sequence 57, App1
33	941	37.8	161	4	US-09-326-394-2	Sequence 2, App11
34	904	36.3	154	4	US-08-828-683a-12	Sequence 12, App1
35	900	36.2	153	2	US-08-219-237b-4	Sequence 4, App11
36	900	36.2	153	4	US-08-476-862-3	Sequence 12, App1
37	900	36.2	153	4	US-08-476-862-3	Sequence 3, App11
38	900	36.2	153	4	US-08-468-560C-4	Sequence 4, App11
39	873	35.1	154	2	US-08-332-087a-10	Sequence 10, App1
40	861	34.6	307	4	US-08-804-166-4	Sequence 4, App11
41	861	34.6	307	4	US-08-910-991-4	Sequence 4, App11
42	854.5	34.4	158	1	US-08-050-319b-54	Sequence 54, App1
43	854.5	34.4	158	4	US-08-465-982-54	Sequence 54, App1
44	842.5	33.9	256	4	US-08-804-166-2	Sequence 2, App11
45	842.5	33.9	256	4	US-08-910-991-2	Sequence 2, App11

ALIGNMENTS

RESULT 1
US-08-321-668-2
Sequence 2, Application US/08321668
Patent No. 5665859
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARTOLOMEY, Eugene
APPLICANT: BARKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-Oct-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-Oct-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-321-668-2
Query Match 100.0%; Score 2487; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 8,9e+203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGSTVDPDLLPLVLELLVGIIPSGVIGLVPHLGDREKRDVCPGKXIHPONNISCTT 60
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DB 61 KCHKGTLYLNDGPGQDDPCRECSGSFTASENHLRHCLSCSKCKREMGQVEISSCTVD 120
QY 121 RDTVCGCRNORYRHVSENLFOCFNCSLCLNGTVHLSCEKONTVCTCHAGFFLRENECY 180
DB 121 RDTVCGCRNORYRHVSENLFOCFNCSLCLNGTVHLSCEKONTVCTCHAGFFLRENECY 180
QY 181 SCGNCKKSLECKTKLPQIENKAGTDSCTVLLPLVIFFGICLISLFTGLMYRYQRWK 240
DB 181 SCGNCKKSLECKTKLPQIENKAGTDSCTVLLPLVIFFGICLISLFTGLMYRYQRWK 240
QY 241 SKLYSVCGKSTPEKEGELGGTTTKPLAPNPSPTPGFTPLGFSVPSSFTSSSTYT 300
DB 241 SKLYSVCGKSTPEKEGELGGTTTKPLAPNPSPTPGFTPLGFSVPSSFTSSSTYT 300
QY 301 PGDCPFPAAPRREVAPPYGADPILATALASDPINPPLQKWEBSAKHPOSLOTDPAATLY 360
DB 301 PGDCPFPAAPRREVAPPYGADPILATALASDPINPPLQKWEBSAKHPOSLOTDPAATLY 360
QY 361 AVVENPPLRMKEFVRLGLSDHEIDRLBLONGRCLEAQSMLATWRRTTREATLEL 420
DB 361 AVVENPPLRMKEFVRLGLSDHEIDRLBLONGRCLEAQSMLATWRRTTREATLEL 420
QY 421 LGRVLRMDLGLCLEDIEBALCPALPPAPSLR 455
DB 421 LGRVLRMDLGLCLEDIEBALCPALPPAPSLR 455

RESULT 2
US-08-837-941-2
; Sequence 2, Application US/08837941
; Patent No. 5766917
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEY, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TMR RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,941
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/321,668
; FILING DATE: 12-OCT-1994
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
; TELE: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-837-941-2
Query Match 100.0%; Score 2487; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSTVDPDLLPLVLELLVGIIPSGVIGLVPHLGDREKRDVCPGKXIHPONNISCTT 60
DB 1 MGSTVDPDLLPLVLELLVGIIPSGVIGLVPHLGDREKRDVCPGKXIHPONNISCTT 60
QY 61 KCHKGTLYLNDGPGQDDPCRECSGSFTASENHLRHCLSCSKCKREMGQVEISSCTVD 120
DB 61 KCHKGTLYLNDGPGQDDPCRECSGSFTASENHLRHCLSCSKCKREMGQVEISSCTVD 120
QY 121 RDTVCGCRNORYRHVSENLFOCFNCSLCLNGTVHLSCEKONTVCTCHAGFFLRENECY 180
DB 121 RDTVCGCRNORYRHVSENLFOCFNCSLCLNGTVHLSCEKONTVCTCHAGFFLRENECY 180
QY 181 SCGNCKKSLECKTKLPQIENKAGTDSCTVLLPLVIFFGICLISLFTGLMYRYQRWK 240
DB 181 SCGNCKKSLECKTKLPQIENKAGTDSCTVLLPLVIFFGICLISLFTGLMYRYQRWK 240
QY 241 SKLYSVCGKSTPEKEGELGGTTTKPLAPNPSPTPGFTPLGFSVPSSFTSSSTYT 300
DB 241 SKLYSVCGKSTPEKEGELGGTTTKPLAPNPSPTPGFTPLGFSVPSSFTSSSTYT 300
QY 301 PGDCPFPAAPRREVAPPYGADPILATALASDPINPPLQKWEBSAKHPOSLOTDPAATLY 360
DB 301 PGDCPFPAAPRREVAPPYGADPILATALASDPINPPLQKWEBSAKHPOSLOTDPAATLY 360
QY 361 AVVENPPLRMKEFVRLGLSDHEIDRLBLONGRCLEAQSMLATWRRTTREATLEL 420
DB 361 AVVENPPLRMKEFVRLGLSDHEIDRLBLONGRCLEAQSMLATWRRTTREATLEL 420
QY 421 LGRVLRMDLGLCLEDIEBALCPALPPAPSLR 455
DB 421 LGRVLRMDLGLCLEDIEBALCPALPPAPSLR 455

RESULT 3
US-08-126-016-2
; Sequence 2, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
; APPLICANT: WALLACH, DAVID
; APPLICANT: NOPAR, YARON
; APPLICANT: KEMPER, OLIVER
; APPLICANT: ENGELMANN, HARTMUT
; APPLICANT: BRAKEBUSCH, CORD
; APPLICANT: ADERKA, DAN
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126,016
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/625668
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-126-016-2

Query Match      100.0%; Score 2487; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 8,9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVDDLPLVLLLELVGIVPSGVIGLVPHLGDRKRDVCPQCKYIHPONNISICT 60
DB 1 MGLSTVDDLPLVLLLELVGIVPSGVIGLVPHLGDRKRDVCPQCKYIHPONNISICT 60
QY 61 KCHKGYLYNDCCPGGDDTDCRECESSGFTASENHLRHCLSCSKRREMGVEISSCTVD 120
DB 61 KCHKGYLYNDCCPGGDDTDCRECESSGFTASENHLRHCLSCSKRREMGVEISSCTVD 120
QY 121 RDYVCGCRKNQYRHYWSENLFQCFNCISCLNGVTHLSQOEKQNTVCCHGFFIRENCEV 180
DB 121 RDYVCGCRKNQYRHYWSENLFQCFNCISCLNGVTHLSQOEKQNTVCCHGFFIRENCEV 180
QY 181 SCSNCKKSLLECTKLCPLQIENVKGTEDSGTTLPLVIFFGICLLSLFTGLMTRYORWK 240
DB 181 SCSNCKKSLLECTKLCPLQIENVKGTEDSGTTLPLVIFFGICLLSLFTGLMTRYORWK 240
QY 241 SKLYSIYCGKSTPEKEBELGTTTKPLAPNPSFSPGFTPTLGFSPVPSSTFTSSSTYT 300
DB 241 SKLYSIYCGKSTPEKEBELGTTTKPLAPNPSFSPGFTPTLGFSPVPSSTFTSSSTYT 300
QY 301 PGDCPNFAAPRREVAAPYOGADPILATALASDPIPNPLQKWEBSAHKPOSLDTPDPAITLY 360
DB 301 PGDCPNFAAPRREVAAPYOGADPILATALASDPIPNPLQKWEBSAHKPOSLDTPDPAITLY 360
QY 361 AVVENVPPLRWKEFVRRLGSLDHEIDRLQLONGRCLREAOYSMLATWRRTPRREATLEL 420
DB 361 AVVENVPPLRWKEFVRRLGSLDHEIDRLQLONGRCLREAOYSMLATWRRTPRREATLEL 420
QY 421 LGRVLRMDLGLCLEDIEBALCGPALPAPASLLR 455
DB 421 LGRVLRMDLGLCLEDIEBALCGPALPAPASLLR 455

```

```

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HERewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: NO. 6153402 yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steife, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
;
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-815-469-5

Query Match      100.0%; Score 2487; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 8,9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVDDLPLVLLLELVGIVPSGVIGLVPHLGDRKRDVCPQCKYIHPONNISICT 60
DB 1 MGLSTVDDLPLVLLLELVGIVPSGVIGLVPHLGDRKRDVCPQCKYIHPONNISICT 60
QY 61 KCHKGYLYNDCCPGGDDTDCRECESSGFTASENHLRHCLSCSKRREMGVEISSCTVD 120
DB 61 KCHKGYLYNDCCPGGDDTDCRECESSGFTASENHLRHCLSCSKRREMGVEISSCTVD 120
QY 121 RDYVCGCRKNQYRHYWSENLFQCFNCISCLNGVTHLSQOEKQNTVCCHGFFIRENCEV 180
DB 121 RDYVCGCRKNQYRHYWSENLFQCFNCISCLNGVTHLSQOEKQNTVCCHGFFIRENCEV 180
QY 181 SCSNCKKSLLECTKLCPLQIENVKGTEDSGTTLPLVIFFGICLLSLFTGLMTRYORWK 240
DB 181 SCSNCKKSLLECTKLCPLQIENVKGTEDSGTTLPLVIFFGICLLSLFTGLMTRYORWK 240
QY 241 SKLYSIYCGKSTPEKEBELGTTTKPLAPNPSFSPGFTPTLGFSPVPSSTFTSSSTYT 300
DB 241 SKLYSIYCGKSTPEKEBELGTTTKPLAPNPSFSPGFTPTLGFSPVPSSTFTSSSTYT 300
QY 301 PGDCPNFAAPRREVAAPYOGADPILATALASDPIPNPLQKWEBSAHKPOSLDTPDPAITLY 360
DB 301 PGDCPNFAAPRREVAAPYOGADPILATALASDPIPNPLQKWEBSAHKPOSLDTPDPAITLY 360
QY 361 AVVENVPPLRWKEFVRRLGSLDHEIDRLQLONGRCLREAOYSMLATWRRTPRREATLEL 420
DB 361 AVVENVPPLRWKEFVRRLGSLDHEIDRLQLONGRCLREAOYSMLATWRRTPRREATLEL 420
QY 421 LGRVLRMDLGLCLEDIEBALCGPALPAPASLLR 455

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DB 421 LGRVLRMDMLGCLDEDIEEALCGPALPPAPSLR 455

RESULT 5
US-09-006-353A-3
Sequence 3, Application US/09006353A

Patent No. 6261801

GENERAL INFORMATION:

APPLICANT: WEI, YING-FEI

APPLICANT: YU, GUO-LIANG

APPLICANT: GENTZ, REINER

APPLICANT: RUBEN, STEVEN

TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/006,353A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF341

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 455 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-006-353A-3

Query Match 100.0%; Score 2487; DB 4; Length 455;

Best Local Similarity 100.0%; Pred. No. 8.9e-203;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXIIHPQNNISICT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXIIHPQNNISICT 60
QY 61 KKHKGTYLVNDPGRQDTCRECSGSFTASENHLRHCLSCSKCKKMGQVEISSCTVD 120
DB 61 KKHKGTYLVNDPGRQDTCRECSGSFTASENHLRHCLSCSKCKKMGQVEISSCTVD 120
QY 121 RDTVCGCRKNOYRHYWSENLFOCFNCISCLNGTVHLSCEKONTVCTCAGFFLRENECV 180
DB 121 RDTVCGCRKNOYRHYWSENLFOCFNCISCLNGTVHLSCEKONTVCTCAGFFLRENECV 180
QY 181 SCSSNCKKSLCTKLCPLQIENYKGTEDSGTVLLPLVIFGCLLSLFIGLMYRYQRMK 240
DB 181 SCSSNCKKSLCTKLCPLQIENYKGTEDSGTVLLPLVIFGCLLSLFIGLMYRYQRMK 240
QY 241 SKLYSIYVCKSTPEKKEGELGTTTKPLAPNPSFPTPGTPTPLGSPVPSSTFTSSSTYT 300
DB 241 SKLYSIYVCKSTPEKKEGELGTTTKPLAPNPSFPTPGTPTPLGSPVPSSTFTSSSTYT 300
QY 301 PDCDFNFAAPREVAAPPYOGADPILATALASDPIPNPLOKWDSDAHKQPSLTDTPATLY 360
DB 301 PDCDFNFAAPREVAAPPYOGADPILATALASDPIPNPLOKWDSDAHKQPSLTDTPATLY 360

DB 301 PDCDFNFAAPREVAAPPYOGADPILATALASDPIPNPLOKWDSDAHKQPSLTDTPATLY 360

QY 361 AVVENVPLRMKEFEVRLGLSDHEIDRLQLONGRCLEAOYSMLATWRRRTPREATLEL 420
DB 361 AVVENVPLRMKEFEVRLGLSDHEIDRLQLONGRCLEAOYSMLATWRRRTPREATLEL 420

QY 421 LGRVLRMDMLGCLDEDIEEALCGPALPPAPSLR 455

DB 421 LGRVLRMDMLGCLDEDIEEALCGPALPPAPSLR 455

RESULT 6
US-09-527-236A-5
Sequence 5, Application US/09527236A

Patent No. 6358508

GENERAL INFORMATION:

APPLICANT: NI, Jian

APPLICANT: Yu, Guo-Liang

APPLICANT: Fan, Ping

APPLICANT: Gentz, Reiner L.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9

FILE REFERENCE: PF375P1

CURRENT APPLICATION NUMBER: US/09/527,236A

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 1997-06-11

PRIOR FILING DATE: 1997-06-11

PRIOR FILING DATE: 1998-06-10

PRIOR FILING DATE: 1998-06-10

PRIOR FILING DATE: 1999-03-24

PRIOR FILING DATE: 1999-03-24

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 5

LENGTH: 455

TYPE: PRT

ORGANISM: Homo sapiens

US-09-527-236A-5

Query Match 100.0%; Score 2487; DB 4; Length 455;

Best Local Similarity 100.0%; Pred. No. 8.9e-203;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXIIHPQNNISICT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXIIHPQNNISICT 60
QY 61 KKHKGTYLVNDPGRQDTCRECSGSFTASENHLRHCLSCSKCKKMGQVEISSCTVD 120
DB 61 KKHKGTYLVNDPGRQDTCRECSGSFTASENHLRHCLSCSKCKKMGQVEISSCTVD 120
QY 121 RDTVCGCRKNOYRHYWSENLFOCFNCISCLNGTVHLSCEKONTVCTCAGFFLRENECV 180
DB 121 RDTVCGCRKNOYRHYWSENLFOCFNCISCLNGTVHLSCEKONTVCTCAGFFLRENECV 180
QY 181 SCSSNCKKSLCTKLCPLQIENYKGTEDSGTVLLPLVIFGCLLSLFIGLMYRYQRMK 240
DB 181 SCSSNCKKSLCTKLCPLQIENYKGTEDSGTVLLPLVIFGCLLSLFIGLMYRYQRMK 240
QY 241 SKLYSIYVCKSTPEKKEGELGTTTKPLAPNPSFPTPGTPTPLGSPVPSSTFTSSSTYT 300
DB 241 SKLYSIYVCKSTPEKKEGELGTTTKPLAPNPSFPTPGTPTPLGSPVPSSTFTSSSTYT 300
QY 301 PDCDFNFAAPREVAAPPYOGADPILATALASDPIPNPLOKWDSDAHKQPSLTDTPATLY 360
DB 301 PDCDFNFAAPREVAAPPYOGADPILATALASDPIPNPLOKWDSDAHKQPSLTDTPATLY 360
QY 361 AVVENVPLRMKEFEVRLGLSDHEIDRLQLONGRCLEAOYSMLATWRRRTPREATLEL 420
DB 361 AVVENVPLRMKEFEVRLGLSDHEIDRLQLONGRCLEAOYSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDMLGCLDEDIEEALCGPALPPAPSLR 455
DB 421 LGRVLRMDMLGCLDEDIEEALCGPALPPAPSLR 455

Db 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455

RESULT 7
US-08-054-970-2
Sequence 2, Application US/08054970

Patent No. 6395267
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/054,970
FILING DATE: 03-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-054-970-2

Query Match 100.0%; Score 2487; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDLLPLVLELLVGIYPSGVIIGLVPHLGDREKRDSDYCPQKXTHPONNSICT 60
Db 1 MGISTVPDLLPLVLELLVGIYPSGVIIGLVPHLGDREKRDSDYCPQKXTHPONNSICT 60
QY 61 KCHKGITLYNDCCPGDDTDCRECESSGFTASENHLRHCLSCSKCKREKMGQVEISSCTVD 120
Db 61 KCHKGITLYNDCCPGDDTDCRECESSGFTASENHLRHCLSCSKCKREKMGQVEISSCTVD 120
QY 121 RDVYCGCRKNQRYHYSENLFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFLRENECV 180
Db 121 RDVYCGCRKNQRYHYSENLFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFLRENECV 180
QY 181 SCNSCKSLSECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRQRMK 240
Db 181 SCNSCKSLSECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRQRMK 240
QY 241 SKLYSTYCGSTPEKEBELGTTTKPLAPNPSFPTGFTPTLGFSPVPSSTFTSSSTYT 300
Db 241 SKLYSTYCGSTPEKEBELGTTTKPLAPNPSFPTGFTPTLGFSPVPSSTFTSSSTYT 300
QY 301 PGDCPNFAARREVAAPRYOGADPLATALASDPINPDLQKWEBSAHKPOSIDTDDPATLY 360
Db 301 PGDCPNFAARREVAAPRYOGADPLATALASDPINPDLQKWEBSAHKPOSIDTDDPATLY 360

QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEADQYSLMATWRRTTTPREATLEL 420
Db 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEADQYSLMATWRRTTTPREATLEL 420
QY 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455
Db 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455

RESULT 8
US-09-565-918-4
Sequence 4, Application US/09565918

Patent No. 6433147
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4
FILE REFERENCE: 1488.1300005
CURRENT APPLICATION NUMBER: US/09/565,918
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,922
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: US 09/013,895
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: US 60/037,829
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: US 60/035,722
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-565-918-4

Query Match 100.0%; Score 2487; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDLLPLVLELLVGIYPSGVIIGLVPHLGDREKRDSDYCPQKXTHPONNSICT 60
Db 1 MGISTVPDLLPLVLELLVGIYPSGVIIGLVPHLGDREKRDSDYCPQKXTHPONNSICT 60
QY 61 KCHKGITLYNDCCPGDDTDCRECESSGFTASENHLRHCLSCSKCKREKMGQVEISSCTVD 120
Db 61 KCHKGITLYNDCCPGDDTDCRECESSGFTASENHLRHCLSCSKCKREKMGQVEISSCTVD 120
QY 121 RDVYCGCRKNQRYHYSENLFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFLRENECV 180
Db 121 RDVYCGCRKNQRYHYSENLFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFLRENECV 180
QY 181 SCNSCKSLSECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRQRMK 240
Db 181 SCNSCKSLSECTKLCPLQIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRQRMK 240
QY 241 SKLYSTYCGSTPEKEBELGTTTKPLAPNPSFPTGFTPTLGFSPVPSSTFTSSSTYT 300
Db 241 SKLYSTYCGSTPEKEBELGTTTKPLAPNPSFPTGFTPTLGFSPVPSSTFTSSSTYT 300
QY 301 PGDCPNFAARREVAAPRYOGADPLATALASDPINPDLQKWEBSAHKPOSIDTDDPATLY 360
Db 301 PGDCPNFAARREVAAPRYOGADPLATALASDPINPDLQKWEBSAHKPOSIDTDDPATLY 360
QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEADQYSLMATWRRTTTPREATLEL 420
Db 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEADQYSLMATWRRTTTPREATLEL 420
QY 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455
Db 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455

DB 421 LGRVLRMDLGLGLEDIEEALCGPALPPAPSLR 455

RESULT 9
US-09-573-986-3
Sequence 3, Application US/09573986
Patent No. 6455040
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Ni, Jian
APPLICANT: Gentz, Steiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280004
CURRENT APPLICATION NUMBER: US/09/573,986
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-573-986-3

Query Match Best Local Similarity 100.0%; Score 2487; DB 4; Length 455;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXTHPQNNISCT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXTHPQNNISCT 60
QY 61 KKHGTYLYNDGPGQDTCRECSGSFTASENHLRHCLSCSKCKEMGOVEISSCTVD 120
DB 61 KKHGTYLYNDGPGQDTCRECSGSFTASENHLRHCLSCSKCKEMGOVEISSCTVD 120
QY 121 RPTVGCGRKNQRYHWSENLFCQFNCISLCLNGTVHLSQOEKQNTVCTCHAGFFLENECV 180
DB 121 RPTVGCGRKNQRYHWSENLFCQFNCISLCLNGTVHLSQOEKQNTVCTCHAGFFLENECV 180
QY 181 SCSNCKKSELECTKLCPLQIENYKGTEDSGTYLLPLVIFFGCLLSLFIGLMYRYORWK 240
DB 181 SCSNCKKSELECTKLCPLQIENYKGTEDSGTYLLPLVIFFGCLLSLFIGLMYRYORWK 240
QY 241 SKLYSIYVGKSTPEKEGELGTTTKPLAPNDSFSPGFTPLGFSVPVSSFTSSSTYT 300
DB 241 SKLYSIYVGKSTPEKEGELGTTTKPLAPNDSFSPGFTPLGFSVPVSSFTSSSTYT 300
QY 301 PGDCNFAPAREVAPPYOGADPILATLASDPIPNPLOKWDNSAHKQSLDTPDPTLY 360
DB 301 PGDCNFAPAREVAPPYOGADPILATLASDPIPNPLOKWDNSAHKQSLDTPDPTLY 360
QY 361 AVVENVPLRMKEFYRRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRRRPREATLEL 420
DB 361 AVVENVPLRMKEFYRRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRRRPREATLEL 420
QY 421 LGRVLRMDLGLGLEDIEEALCGPALPPAPSLR 455
DB 421 LGRVLRMDLGLGLEDIEEALCGPALPPAPSLR 455

RESULT 10
US-08-050-319B-25
Sequence 25, Application US/08050319B
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins

STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-319B-25

Query Match Best Local Similarity 99.8%; Score 2482; DB 1; Length 455;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXTHPQNNISCT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXTHPQNNISCT 60
QY 61 KKHGTYLYNDGPGQDTCRECSGSFTASENHLRHCLSCSKCKEMGOVEISSCTVD 120
DB 61 KKHGTYLYNDGPGQDTCRECSGSFTASENHLRHCLSCSKCKEMGOVEISSCTVD 120
QY 121 RPTVGCGRKNQRYHWSENLFCQFNCISLCLNGTVHLSQOEKQNTVCTCHAGFFLENECV 180
DB 121 RPTVGCGRKNQRYHWSENLFCQFNCISLCLNGTVHLSQOEKQNTVCTCHAGFFLENECV 180
QY 181 SCSNCKKSELECTKLCPLQIENYKGTEDSGTYLLPLVIFFGCLLSLFIGLMYRYORWK 240
DB 181 SCSNCKKSELECTKLCPLQIENYKGTEDSGTYLLPLVIFFGCLLSLFIGLMYRYORWK 240
QY 241 SKLYSIYVGKSTPEKEGELGTTTKPLAPNDSFSPGFTPLGFSVPVSSFTSSSTYT 300
DB 241 SKLYSIYVGKSTPEKEGELGTTTKPLAPNDSFSPGFTPLGFSVPVSSFTSSSTYT 300
QY 301 PGDCNFAPAREVAPPYOGADPILATLASDPIPNPLOKWDNSAHKQSLDTPDPTLY 360
DB 301 PGDCNFAPAREVAPPYOGADPILATLASDPIPNPLOKWDNSAHKQSLDTPDPTLY 360
QY 361 AVVENVPLRMKEFYRRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRRRPREATLEL 420
DB 361 AVVENVPLRMKEFYRRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRRRPREATLEL 420
QY 421 LGRVLRMDLGLGLEDIEEALCGPALPPAPSLR 455
DB 421 LGRVLRMDLGLGLEDIEEALCGPALPPAPSLR 455

RESULT 11
US-08-465-982-25
Sequence 25, Application US/08465982
Patent No. 5863786
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M. Brennan

;; TITLE OF INVENTION: Modified human TNFalpha (Tumor
;; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Reed & Robbins
;; STREET: 635 Bryant Street
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94301
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/465,982
;; FILING DATE:
;; CLASSIFICATION:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US/08/050,319
;; FILING DATE: 10-May-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Robbins, Roberta L.
;; REGISTRATION NUMBER: 33,208
;; REFERENCE/DOCKET NUMBER: 5150-0030
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 617-8999
;; TELEFAX: (415) 327-3231
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 455 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-465-982-25
;
Query Match 99.8%; Score 2482; DB 2; Length 455;
Best Local Similarity 99.8%; Pred. No. 2,4e-202;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDERKDSVCPQKTYHPONNSICT 60
DB 1 MGSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDERKDSVCPQKTYHPONNSICT 60
QY 61 KCHKGTLYNDGPGGDDTCRCESGSPYASENHLRHCLSCSKRKEKMGVEISSCTVD 120
DB 61 KCHKGTLYNDGPGGDDTCRCESGSPYASENHLRHCLSCSKRKEKMGVEISSCTVD 120
QY 121 RDVTGCGRRKQYRHYWSENLFQCFNCSLCINGVHLSCEKONTVCTCHAGFFLRENECV 180
DB 121 RDVTGCGRRKQYRHYWSENLFQCFNCSLCINGVHLSCEKONTVCTCHAGFFLRENECV 180
QY 181 SCNSCKSLCTKLCIPQLEINVKGTEDSGTIVLLPLVIFFGICLSLFTGLMYRYQRW 240
DB 181 SCNSCKSLCTKLCIPQLEINVKGTEDSGTIVLLPLVIFFGICLSLFTGLMYRYQRW 240
QY 241 SKLYSIVCGSTPEKEGELGGTTTKPLAPNPSFPTPGFTPTLGFSPVSSSTFTSSTYT 300
DB 241 SKLYSIVCGSTPEKEGELGGTTTKPLAPNPSFPTPGFTPTLGFSPVSSSTFTSSTYT 300
QY 301 PGDCPNAPARREYAPPYQADPLATATLASDPIPNPLQKWEDSAHKPOSIDTDDPATLY 360
DB 301 PGDCPNAPARREYAPPYQADPLATATLASDPIPNPLQKWEDSAHKPOSIDTDDPATLY 360
QY 361 AVVENVPLRMKEFVRRLGSDHEIDRLONGRCLEADQYSMATYRRRRTPREATLEL 420
DB 361 AVVENVPLRMKEFVRRLGSDHEIDRLONGRCLEADQYSMATYRRRRTPREATLEL 420
QY 421 LGRVLRMDMLGCLIEDIEEALCGPAALPPAPSLLR 455
DB 421 LGRVLRMDMLGCLIEDIEEALCGPAALPPAPSLLR 455

RESULT 12
US-09-013-895A-4
; Sequence 4, Application US/09013895A
; Patent No. 6342363
;; GENERAL INFORMATION:
;; APPLICANT: NI, Jian
;; APPLICANT: Rosen, Craig A.
;; APPLICANT: Pan, James G.
;; APPLICANT: Gentz, Reiner L.
;; APPLICANT: Dixit, Vishva M.
;; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
;; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
;; STREET: 9410 KEY WEST AVENUE
;; CITY: ROCKVILLE
;; STATE: MD
;; COUNTRY: US
;; ZIP: 20850
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/013,895A
;; FILING DATE: 27-JAN-1998
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEFFE, ERIC K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.1300002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 909 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-013-895A-4
;
Query Match 99.1%; Score 2463.5; DB 4; Length 909;
Best Local Similarity 99.3%; Pred. No. 2.2e-200;
Matches 453; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDERKDSVCPQKTYHPONNSICT 60
DB 454 MGSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDERKDSVCPQKTYHPONNSICT 513
QY 61 KCHKGTLYNDGPGGDDTCRCESGSPYASENHLRHCLSCSKR-KEKMGVEISSCTV 119
DB 61 KCHKGTLYNDGPGGDDTCRCESGSPYASENHLRHCLSCSKRKEKMGVEISSCTV 119
QY 120 DRDTVCGCRKQYRHYWSENLFQCFNCSLCINGVHLSCEKONTVCTCHAGFFLRENEC 179
DB 120 DRDTVCGCRKQYRHYWSENLFQCFNCSLCINGVHLSCEKONTVCTCHAGFFLRENEC 179
QY 180 VSCSNCKSLCTKLCIPQLEINVKGTEDSGTIVLLPLVIFFGICLSLFTGLMYRYQRW 239
DB 180 VSCSNCKSLCTKLCIPQLEINVKGTEDSGTIVLLPLVIFFGICLSLFTGLMYRYQRW 239
QY 240 KSKLYSIVCGSTPEKEGELGGTTTKPLAPNPSFPTPGFTPTLGFSPVSSSTFTSSTYT 299
DB 240 KSKLYSIVCGSTPEKEGELGGTTTKPLAPNPSFPTPGFTPTLGFSPVSSSTFTSSTYT 299
QY 299 KSKLYSIVCGSTPEKEGELGGTTTKPLAPNPSFPTPGFTPTLGFSPVSSSTFTSSTYT 359
DB 299 KSKLYSIVCGSTPEKEGELGGTTTKPLAPNPSFPTPGFTPTLGFSPVSSSTFTSSTYT 359

Db 754 TPDCPNFAAPRREVAAPYOGADPILATATLASDPIPNPLQKWDASHKQSDTDDPATL 813
Qy 360 YAVENVPPLRKKEFYRRIGLSDEIDRLONGRCLREAOYSMLATWRRRPREATE 419
Db 814 YAVENVPPLRKKEFYRRIGLSDEIDRLONGRCLREAOYSMLATWRRRPREATE 873
Qy 420 LIGRVLROMDLGLCLEDIEALCGPALPPAPSLR 455
Db 874 LIGRVLROMDLGLCLEDIEALCGPALPPAPSLR 909

RESULT 13

US-09-448-868-4
; Sequence 4, Application US/09448868
; Patent No. 6461823
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (Ap02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 909 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-448-868-4

Query Match 99.1%; Score 2463.5; DB 4; Length 909;
Best Local Similarity 99.3%; Pred. No. 2.2e-200;
Matches 453; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MGLSTVPDLLPLVLTLELVGIVPGVIGLVPHLGDRKRDVSCPOGKIYHONNSICT 60
Db 454 MGLSTVPDLLPLVLTLELVGIVPGVIGLVPHLGDRKRDVSCPOGKIYHONNSICT 513
Qy 61 KCHKGTIYLNDCPGPGQDTCRECESSGFTASENHLRHCLSCSKCR-KEMGOVEISSCTV 119
Db 514 KCHKGTIYLNDCPGPGQDTCRECESSGFTASENHLRHCLSCSKCRKEMGOVEISSCTV 573

Qy 120 DRDTVCGCRKNQYRHYSENLFQCFNCISCLNGTVHLSQOEQONTVCTCHAGFELRENEC 179
Db 574 DRDTVCGCRKNQYRHYSENLFQCFNCISCLNGTVHLSQOEQONTVCTCHAGFELRENEC 633
Qy 180 VSCSNCKKSLCTCKLCPLEIENKVGTEDESGTTLPLVTFVFGCLSLFLIGLAMYORW 239
Db 634 VSCSNCKKSLCTCKLCPLEIENKVGTEDESGTTLPLVTFVFGCLSLFLIGLAMYORW 693
Qy 240 KSKLYSIVCGKSTPEKEGELGTTKPLAPNPSFPTPTLGRSPVSSSTFTSSSTY 299
Db 694 KSKLYSIVCGKSTPEKEGELGTTKPLAPNPSFPTPTLGRSPVSSSTFTSSSTY 753
Qy 300 TPDCPNFAAPRREVAAPYOGADPILATATLASDPIPNPLQKWDASHKQSDTDDPATL 359
Db 754 TPDCPNFAAPRREVAAPYOGADPILATATLASDPIPNPLQKWDASHKQSDTDDPATL 813
Qy 360 YAVENVPPLRKKEFYRRIGLSDEIDRLONGRCLREAOYSMLATWRRRPREATE 419
Db 814 YAVENVPPLRKKEFYRRIGLSDEIDRLONGRCLREAOYSMLATWRRRPREATE 873
Qy 420 LIGRVLROMDLGLCLEDIEALCGPALPPAPSLR 455
Db 874 LIGRVLROMDLGLCLEDIEALCGPALPPAPSLR 909

RESULT 14

US-09-086-483A-5
; Sequence 5, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PP379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-086-483A-5

Query Match 98.8%; Score 2457; DB 4; Length 453;
 Best Local Similarity 99.6%; Pred. No. 3,1e-200;
 Matches 453; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MGLSTVPDLPLPLVLELVGIVPSGVIGLPHLGDRKRDVCPQCKYIHPONNSICT 60
 DB 1 MGLSTVPDLPLPLVLELVGIVPSGVIGLPHLGDRKRDVCPQCKYIHPONNSICT 58
 QY 61 KCHKGTLYLNDPCPGQDPTDCRECESSGSPFASENHLRHCLSCSKRREMGVEISSCTVD 120
 DB 59 KCHKGTLYLNDPCPGQDPTDCRECESSGSPFASENHLRHCLSCSKRREMGVEISSCTVD 118
 QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCISCLNGTVHLSQEQKONTVCTCHAGFFLRENECV 180
 DB 119 RDTVCGCRKNQYRHYWSENLFQCFNCISCLNGTVHLSQEQKONTVCTCHAGFFLRENECV 178
 QY 181 SCNNCKSLECKTLCCLPOIENVKGTEDSGTTLPLVIFPGCLLSLFLIGLAMYRYORWK 240
 DB 179 SCNNCKSLECKTLCCLPOIENVKGTEDSGTTLPLVIFPGCLLSLFLIGLAMYRYORWK 238
 QY 241 SKLYSIVCGKSTPEKEGELGEGTTTKPLAPNPSFSPPTGFTPLGFSPPVSSFTSSSTYT 300
 DB 239 SKLYSIVCGKSTPEKEGELGEGTTTKPLAPNPSFSPPTGFTPLGFSPPVSSFTSSSTYT 298
 QY 301 PGDCPNFAAPRREYAPRYQADPILATKASDPIPNPLQKEDSAHKRQSLDTPDPAITLY 360
 DB 299 PGDCPNFAAPRREYAPRYQADPILATKASDPIPNPLQKEDSAHKRQSLDTPDPAITLY 358
 QY 361 AVENVPPLRKKEFYVRRLGSDHEIDRLONGRCLREAOYSMLATWRPRRREATLEL 420
 DB 359 AVENVPPLRKKEFYVRRLGSDHEIDRLONGRCLREAOYSMLATWRPRRREATLEL 418
 QY 421 LGRVLKRDMDLLGCLLEIEALCGPALPPAPSLR 455
 DB 419 LGRVLKRDMDLLGCLLEIEALCGPALPPAPSLR 453

RESULT 15
 US-08-974-022-46
 ; Sequence 46, Application US/08974022
 ; Patent No. 6015938
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William J.
 ; APPLICANT: Lacey, David L.
 ; APPLICANT: Calzone, Frank J.
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: OSTEOPROTEGERIN
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: 1840 Dehavenland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,022
 ; FILING DATE: 12-DEC-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/577,788
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Winter, Robert B.
 ; REFERENCE/DOCKET NUMBER: A-378
 ; INFORMATION FOR SEQ ID NO: 46:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 280 amino acids

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-974-022-46

Query Match 62.6%; Score 1558; DB 3; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.4e-124;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLPLPLVLELVGIVPSGVIGLPHLGDRKRDVCPQCKYIHPONNSICT 60
 DB 1 MGLSTVPDLPLPLVLELVGIVPSGVIGLPHLGDRKRDVCPQCKYIHPONNSICT 60
 QY 61 KCHKGTLYLNDPCPGQDPTDCRECESSGSPFASENHLRHCLSCSKRREMGVEISSCTVD 120
 DB 61 KCHKGTLYLNDPCPGQDPTDCRECESSGSPFASENHLRHCLSCSKRREMGVEISSCTVD 120
 QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCISCLNGTVHLSQEQKONTVCTCHAGFFLRENECV 180
 DB 121 RDTVCGCRKNQYRHYWSENLFQCFNCISCLNGTVHLSQEQKONTVCTCHAGFFLRENECV 180
 QY 181 SCNNCKSLECKTLCCLPOIENVKGTEDSGTTLPLVIFPGCLLSLFLIGLAMYRYORWK 240
 DB 181 SCNNCKSLECKTLCCLPOIENVKGTEDSGTTLPLVIFPGCLLSLFLIGLAMYRYORWK 240
 QY 241 SKLYSIVCGKSTPEKEGELGEGTTTKPLAPNPSFSPPTGFT 280
 DB 241 SKLYSIVCGKSTPEKEGELGEGTTTKPLAPNPSFSPPTGFT 280

Search completed: December 27, 2002, 15:09:03
 Job time : 19 secs

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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:07:00 ; Search time 21 Seconds
(without alignments)
2082.912 Million cell updates/sec

Title: US-09-899-429a-2

Perfect score: 2487
Sequence: 1 MGSTVPLDLLPLVLELLV.....DIEALGPALPPAPSLR 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2487	100.0	455	1 GQHUT1	tumor necrosis fac
2	1738	69.9	461	2 JCACT02	tumor necrosis fac
3	1563.5	62.9	461	1 GORCT1	tumor necrosis fac
4	1521	61.2	454	1 GOMST1	tumor necrosis fac
5	251.5	10.1	435	2 IS4182	tumor necrosis fac
6	240.5	9.7	427	1 GQHUN	nerve growth facto
7	223	9.0	425	1 A26431	nerve growth facto
8	205	8.2	474	2 B38634	tumor necrosis fac
9	204.5	8.2	459	2 I48854	gene murine tumour
10	200	8.0	326	1 GQVZML	72 protein - myxom
11	196.5	7.9	416	1 JN0006	nerve growth facto
12	192	7.7	325	2 B43692	12 protein - rabbi
13	189.5	7.6	327	2 A46484	apoptosis-mediatin
14	186.5	7.5	651	2 JCT705	death receptor-6 -
15	183.5	7.4	461	1 A35356	tumor necrosis fac
16	177	7.1	335	2 A40036	apoptosis-mediatin
17	176.5	7.1	305	2 A46476	B cell-associated
18	174	7.0	324	2 JCR295	Fas antigen precur
19	166.5	6.7	277	2 A60771	B-cell activation
20	166.5	6.7	349	2 D72175	G2R protein - vari
21	164	6.6	348	2 T28623	hypothetical prote
22	164	6.6	349	2 D36858	gene GAR protein -
23	158	6.4	260	1 A46517	CD27 antigen precu
24	157.5	6.3	314	2 I37383	FAS soluble protei
25	154.5	6.2	355	2 A42086	CD30 antigen precu
26	154	6.2	677	2 C42125	trophozoite cyatel
27	148	6.0	1548	2 S34583	serine proteinase
28	145.5	5.9	837	2 S43566	furin (EC 3.4.21.7
29	143.5	5.8	1680	2 A43434	furin (EC 3.4.21.7

30	143	5.7	250	1 A49053	CD27 antigen precu
31	140	5.6	2824	2 T22759	hypothetical prote
32	136.5	5.5	272	2 I48700	gene ox40 protein
33	133.5	5.4	271	2 S12783	OX40 antigen precu
34	132.5	5.3	899	2 G02428	subtilisin-like pr
35	132.5	5.3	915	2 JC6148	subtilisin-like pr
36	131.5	5.3	826	2 A60385	monocyte surface a
37	130.5	5.2	3672	2 T23433	hypothetical prote
38	130.5	5.2	3704	2 T37316	probable laminin a
39	126.5	5.1	728	2 A48830	probable transcrip
40	124.5	5.0	277	2 T37552	OX40 homolog - hum
41	124	5.0	468	2 S26741	T-cell glycoprotei
42	124	5.0	884	2 T18649	hypothetical prote
43	122.5	4.9	192	2 T25513	hypothetical prote
44	122.5	4.9	213	2 S25647	ookinete surface p
45	121.5	4.9	1299	2 T43251	furin (EC 3.4.21.7

ALIGNMENTS

RESULT 1
GOHUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N:Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 08-Dec-2000
C:Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; J0758; A60231;
R:Frucht, P.; Strehl, S.; Dvorzak, M.; Hummler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to
A:Reference number: A38208; MUID:92250049; PMID:1315717
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <RUC>
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PID:AAA61201.1; PI
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tachsch, H.; Less
Cell 61, 351-359, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor re
A:Reference number: A34899; MUID:90235284; PMID:2158862
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOE>
A:Cross-references: GB:M58286; GB:M33480; NID:g339753; PID:AAA36753.1; PID:g339754
A:Experimental source: Placenta
A:Note: part of this sequence, including the amino end of the mature protein, confirm
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis fact
A:Reference number: A34900; MUID:90235285; PMID:2158863
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:A33294; NID:g339744; PID:AAA03210.1; PID:g339745
R:Hummler, A.; Maurer-Fogy, I.; Krenke, M.; Scheutrich, P.; Pfizenmaier, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:g339755; PID:AAA36754.1; PID:g339756
A:Accession: C36555
A:Molecule type: protein
A:Note: the purified protein, called tumor necrosis factor binding protein, is a solu
R:Gray, P.W.; Barrett, K.; Chantley, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A:Reference number: A38281; MUID:91012509; PMID:2170974
A:Accession: A38281
A:Molecule type: mRNA

A:Residues: 1-455 <GRA>
A:Cross-references: GB:M37764
A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R.Noplat, Y.; Kemper, O.; Bräkebusch, C.; Engemann, H.; Zwaag, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
I le form of the receptor.
A:Reference number: S12057; MUID:91006021; PMID:1698610
A:Accession: S12057
A:Molecule type: mRNA
A:Residues: 1-455 <NOP>
A:Cross-references: EMBL:X55313; NID:q37223; PIDN:CAA39021.1; PID:q37224
R.Noplat, Y.; Kemper, O.; Bräkebusch, C.; Engemann, H.; Zwaag, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A:Title: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
Gene 134, 209-216, 1993
R.Kemper, O.; Wallach, D.
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A:Reference number: J70758; MUID:94085779; PMID:8262379
A:Accession: J70758
A:Molecule type: DNA
A:Residues: 1-13 <KEM>
R.Secklinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
A:Reference number: A60231; MUID:90292116; PMID:2113477
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
R.Gatnaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
tients.
A:Reference number: A38258; MUID:91062364; PMID:2174164
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Experimental source: cancer patient serum
R.Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from
A:Reference number: A60594; MUID:89171156; PMID:2924890
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OIS>
A:Experimental source: renal failure patient urine
R.Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
R.Kirihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biochem. Biotechnol. Biochem. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A:Reference number: J2404; MUID:95128033; PMID:7765720
A:Accession: J2404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/2; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F:44-82/Domain: NGF receptor repeat homology <NGI>

F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
F:54,145,151/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 2487; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.6e-159;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTPDLPLPLVLELLVGIYPSGVILVPLHGBREKDSVCPGKXIIHQNNISCTT 60
|||||
Db 1 MGISTPDLPLPLVLELLVGIYPSGVILVPLHGBREKDSVCPGKXIIHQNNISCTT 60
|||||
QY 61 KCHKGTLYNDCPGPGODTDCRECEGSFTASENHRLHCLSCSKCKEMGOYEISSCTVD 120
|||||
Db 61 KCHKGTLYNDCPGPGODTDCRECEGSFTASENHRLHCLSCSKCKEMGOYEISSCTVD 120
|||||
QY 121 RDTVCGCRNRYRHYWSENLFCFNCISLCLNGTVHLSCEQEKONTVCTCHAGFFLRENECV 180
|||||
Db 121 RDTVCGCRNRYRHYWSENLFCFNCISLCLNGTVHLSCEQEKONTVCTCHAGFFLRENECV 180
|||||
QY 181 SCSNCKKSLIECTKRLCLPQLENNKGTDSSTYVILPLVIFFGCLLSLFTGLMYRQRMK 240
|||||
Db 181 SCSNCKKSLIECTKRLCLPQLENNKGTDSSTYVILPLVIFFGCLLSLFTGLMYRQRMK 240
|||||
QY 241 SKLYSVCKSPKPEKGELEGTTTKPLAPNPSFPPTPLGFSFVPSSTFTSSSTYT 300
|||||
Db 241 SKLYSVCKSPKPEKGELEGTTTKPLAPNPSFPPTPLGFSFVPSSTFTSSSTYT 300
|||||
QY 301 PGDCPFNAAPRRVAPPYGADPILATFALASDPTRPMPLOKWEBSAHKPSQSLTDTPATLY 360
|||||
Db 301 PGDCPFNAAPRRVAPPYGADPILATFALASDPTRPMPLOKWEBSAHKPSQSLTDTPATLY 360
|||||
QY 361 AVEENVPPLRMKEFVRRLGSLSDHEIDRLFLQNGRCLEQYQSMATWRRRTTREATLEL 420
|||||
Db 361 AVEENVPPLRMKEFVRRLGSLSDHEIDRLFLQNGRCLEQYQSMATWRRRTTREATLEL 420
|||||
QY 421 LGRVLRMDMLCLEDIEBALGPAALPPAPSLR 455
|||||
Db 421 LGRVLRMDMLCLEDIEBALGPAALPPAPSLR 455
|||||

RESULT 2
JC4302
tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A:Reference number: JC4302; MUID:96011645; PMID:7590278
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SDU>
A:Cross-references: GB:U19994; NID:g1141752; PIDN:AAC40499.1; PID:g1141753
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SU2>
A:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: tnfr
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:30-461/Product: signal sequence #status predicted <SIG>
F:44-194/Domain: tumor necrosis factor receptor p55 #status predicted <MAT>
F:44-82/Domain: extracellular #status predicted <EXT>
F:84-126/Domain: NGF receptor repeat homology <NGI>
F:211-231/Domain: transmembrane #status predicted <MEM>
F:361-447/Domain: signal transduction #status predicted <STT>

F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.9%; Score 1738; DB 2; Length 461;

Best Local Similarity 71.6%; Pred. No. 9e-109;

Matches 331; Conservative 29; Mismatches 94; Indels 8; Gaps 4;

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QY 1 MGSTVPDLLPLVLELVGIVPSYIGLVPHLGDRKRDSCVCPQCKYIHPPONNSICTT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MGSTVPGLLPLVLRALLDVYVAGVHGLVHPGDRKREKESLCPOCKYSHPPONNSICTT 60
QY 61 KCHKGTYLNDCEPGGDDTDCRECESSFTASENHLRHNCSCSKCKREMOVEISSCTVD 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 KCHKGTYLNDCEPGGDDTDCRECESSFTASENHLRHNCSCSKCKREMOVEISSCTVD 120
QY 121 RDYVCGGRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCYCHAGFFLRENECV 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 RDYVCGGRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCYCHAGFFLRENECV 180
QY 121 RDYVCGGRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCYCHAGFFLRENECV 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 RDYVCGGRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCYCHAGFFLRENECV 180
QY 181 SCNSCKKSLECTKICLPQIENVKCTEDSGTTLPLVIFPGCLLSLFTGLMYRYORWK 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 SCNSCKKSLECTKICLPQIENVKCTEDSGTTLPLVIFPGCLLSLFTGLMYRYORWK 240
QY 241 SKLYSIYCGSTPEKEGELGGTTKP--LADNPSFPTPGFTPLGSPVPSSTFTSSSTY 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 SKLYSIYCGSTPEKEGELGGTTKP--LADNPSFPTPGFTPLGSPVPSSTFTSSSTY 299
QY 240 PKLYSIICGASTPYKKESEPEPLATAPSGFTITPSPIPSPSTFTTSPVPSFISSTPT 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 240 PKLYSIICGASTPYKKESEPEPLATAPSGFTITPSPIPSPSTFTTSPVPSFISSTPT 299
QY 300 TPGDCCPNF--AAPREYAPPYOGADPILATALASDPINPQKWEKDSAHK---PQSLDT 353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TPGDCCPNF--AAPREYAPPYOGADPILATALASDPINPQKWEKDSAHK---PQSLDT 353
QY 300 TPGDCCPNF--AAPREYAPPYOGADPILATALASDPINPQKWEKDSAHK---PQSLDT 353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TPGDCCPNF--AAPREYAPPYOGADPILATALASDPINPQKWEKDSAHK---PQSLDT 353
QY 354 DDPAATLYAVENVPLPKWKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPR 413
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 354 DDPAATLYAVENVPLPKWKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPR 413
QY 360 ADPAATLYAVDGVPTPKWKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTSR 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 360 ADPAATLYAVDGVPTPKWKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTSR 419
QY 414 REATLELGRVLRMDLGLCEDEIEALCGPALPAPSLLR 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 420 REATLELGRVLRMDLGLCEDEIEALCGPALPAPSLLR 461

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RESULT 3

GOMST1

tumor necrosis factor receptor 1 precursor - rat

N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999

C:Accession: B36555

R:Hummer, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lant, M.;

DNA Cell Biol. 9: 705-715, 1990

A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor

A:Accession: B36555

A:Reference number: A36555; MUID:91090841; PMID:1702293

A:Molecule type: mRNA

A:Residues: 1-461 <IHM>

A:Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362

C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>

F:30-211/Domain: extracellular #status predicted <EX>

F:30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>

F:44-84/Domain: NGF receptor repeat homology <NG1>

F:84-126/Domain: NGF receptor repeat homology <NG2>

F:127-167/Domain: NGF receptor repeat homology <NG3>

F:168-204/Domain: NGF receptor repeat homology <NG4>

F:212-234/Domain: transmembrane #status predicted <MEM>

F:235-461/Domain: intracellular #status predicted <INT>

F:34,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.9%; Score 1563.5; DB 1; Length 461;

Best Local Similarity 64.9%; Pred. No. 4e-97;

Matches 294; Conservative 46; Mismatches 104; Indels 9; Gaps 4;

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QY 1 MGSTVPDLLPLVLELVGIVPSYIGLVPHLGDRKRDSCVCPQCKYIHPPONNSICTT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MGSTVPGLLPLVLRALLDVYVAGVHGLVHPGDRKREKESLCPOCKYSHPPONNSICTT 60
QY 61 KCHKGTYLNDCEPGGDDTDCRECESSFTASENHLRHNCSCSKCKREMOVEISSCTVD 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 KCHKGTYLNDCEPGGDDTDCRECESSFTASENHLRHNCSCSKCKREMOVEISSCTVD 120
QY 121 RDYVCGGRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCYCHAGFFLRENECV 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 RDYVCGGRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCYCHAGFFLRENECV 180
QY 121 RDYVCGGRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCYCHAGFFLRENECV 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 RDYVCGGRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCYCHAGFFLRENECV 180
QY 181 SCNSCKKSLECTKICLPQIENVKCTEDSGTTLPLVIFPGCLLSLFTGLMYRYORWK 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 SCNSCKKSLECTKICLPQIENVKCTEDSGTTLPLVIFPGCLLSLFTGLMYRYORWK 240
QY 241 SKLYSIYCGSTPEKEGELGGTTKP--LADNPSFPTPGFTPLGSPVPSSTFTSSSTY 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 SKLYSIYCGSTPEKEGELGGTTKP--LADNPSFPTPGFTPLGSPVPSSTFTSSSTY 299
QY 240 PKLYSIICGASTPYKKESEPEPLATAPSGFTITPSPIPSPSTFTTSPVPSFISSTPT 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 240 PKLYSIICGASTPYKKESEPEPLATAPSGFTITPSPIPSPSTFTTSPVPSFISSTPT 299
QY 353 TDPAATLYAVENVPLPKWKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPR 412
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 353 TDPAATLYAVENVPLPKWKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPR 412
QY 360 ADPAATLYAVDGVPTPKWKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTSR 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 360 ADPAATLYAVDGVPTPKWKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTSR 419
QY 413 REATLELGRVLRMDLGLCEDEIEALCGPALPAPSLLR 445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 420 REATLELGRVLRMDLGLCEDEIEALCGPALPAPSLLR 452

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RESULT 4

GOMST1

tumor necrosis factor receptor 1 precursor - mouse

N:Alternate names: tumor necrosis factor receptor, 55K

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000

C:Accession: A38634; B40254; S16677; S19021; I54532; I57826

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto

A:Reference number: A38634; MUID:91187885; PMID:1849278

A:Molecule type: mRNA

A:Residues: 1-454 <LEM>

A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J

Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f

A:Reference number: A40254; MUID:91246168; PMID:1645445

A:Molecule type: mRNA

A:Residues: 1-454 <G62>

A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826

R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Klisonevich, A.M.; Gray, P.W.; Fel

Eur. J. Immunol. 21, 1649-1656, 1991

A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro

A:Reference number: S16677; MUID:91285014; PMID:1647956

A:Accession: S16677

A:Molecule type: mRNA

A:Residues: 1-454 <BAR>

A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579

R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.

Immunogenetics 34, 338-340, 1991

A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.

A:Reference number: S19021; MUID:92039815; PMID:1657766

A:Accession: S19021

A:Molecule type: mRNA

A:Residues: 1-454 <ROT>

A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849

R:Beo, B.F.

Immunogenetics 39, 450-451, 1994
 A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelial cell 1
 A:Reference number: 154532; MUID:94245292; PMID:8188324
 A:Accession: 154532
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-454 <RES>
 A:Cross-references: GB:L26349; NID:9430732; PIDN:AAA59361.1; PID:9430733
 R:Rothe, J.G.; Bluetmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
 Mol. Immunol. 30, 165-176, 1993
 A:Title: Genomic organization and promoter function of the murine tumor necrosis factor
 A:Reference number: 157826; MUID:93156721; PMID:8381516
 A:Accession: 157826
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393, 'G', 395-454 <RE2>
 A:Cross-references: GB:M76656; NID:9202100; PIDN:AAA40465.1; PID:9202102
 C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (c
 C:Genetics:
 A:Gene: TNFR-2
 A:Introns: 13/3; 65/1; 108/1; 184/2; 210/1; 248/1; 257/3; 353/1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei
 F:1-29/Domains: signal sequence #status predicted <SIG>
 F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
 F:30-212/Domains: extracellular #status predicted <EXT>
 F:44-82/Domains: NGF receptor repeat homology <NG1>
 F:84-126/Domains: NGF receptor repeat homology <NG2>
 F:127-167/Domains: NGF receptor repeat homology <NG3>
 F:168-204/Domains: NGF receptor repeat homology <NG4>
 F:213-235/Domains: transmembrane #status predicted <MEM>
 F:236-454/Domains: intracellular #status predicted <INT>
 F:54,151,202/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 61.2%; Score 1521; DB 1; Length 454;
 Best Local Similarity 65.2%; Pred. No. 2,7e-94;
 Matches 294; Conservative 47; Mismatches 98; Indels 12; Gaps 7;

QY 1 MGISTVDDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVSGPGKTIHQNNSTCCT 60
 DB 1 MGIPVPGILLSLVLLALMGIPHCVTGLVPSLGRKRDVSLCPGKTVSHSKNNISCTT 60
 QY 61 KCHKGTYLVNDCPGPDPTDCRECSGFTASBNHRLHGLSCSKCKEMGOYEISCTVD 120
 DB 61 KCHKGTYLVNDCPGPDPTDCRECSGFTASBNHRLHGLSCSKCKEMGOYEISCTVD 120
 QY 121 RDTVCGCRNORYRHVWSENIPOCFNCISLCLNGTVHLSCEKONTVCTCHAGFLRENECV 180
 DB 121 RDTVCGCRNORYRHVWSENIPOCFNCISLCLNGTVHLSCEKONTVCTCHAGFLRENECV 180
 QY 121 KDTVCGCRNORYRHVWSENIPOCFNCISLCLNGTVHLSCEKONTVCTCHAGFLRENECV 180
 DB 121 KDTVCGCRNORYRHVWSENIPOCFNCISLCLNGTVHLSCEKONTVCTCHAGFLRENECV 180
 QY 181 SCGNCKKSLSECTKLCI-POIENVKGTEDSGTIVLLPLVIFPGICLSLFLIGLMRYORW 239
 DB 181 PSCHCKKNECKKLCIPLPLAVNTNPOSGTAVLLPLVILICLSLFFISILMCRYPW 240
 QY 240 KSKIVSYVCGKSTPEKEGLEGTITKPL--APNPSRSPRTGTPPLGTFSPVSSSTTSS 297
 DB 241 KREVSIICORDPVPAKE-EKAC--KPLPAPSPAPSPSPSGNPTLGFSPGSSSVST 296
 QY 298 TYPGDCP---NFAAPRREAVPYOGADPILATATASDPIPLPLQKWEBSAKRPOSITD 354
 DB 297 PLSPIFGPSNMHFMPPVSVVPT-OGADPLILYESLCSVAPFVSQKWEBSAH-PQRDPA 354
 QY 355 DPATLYAVENVPLRKMEFVRRLGSLDHEIDRLDLONGRCRLREAOYSMLATWRRRTPRR 414
 DB 355 DPAIITYAVDVGPPARWKEFRFMGLSEHIEIRLEKONGRCRLREAOYSMLAEMRRRTPRH 414
 QY 415 EATLELLGVLRDMDLGLGLEDIEEALGCPA 445
 DB 415 EDPLVAVGLVLSKMDLGLGLEDIEEALRNP 445

tumor necrosis factor receptor 2-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
 C:Accession: 154182
 R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
 Genomics 16, 214-218, 1993
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq
 A:Reference number: 154182; MUID:93252381; PMID:8486360
 A:Accession: 154182
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-435 <RES>
 A:Cross-references: GB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762
 C:Genetics:
 A:Gene: LTBR
 A:Cross-references: GDB:1230195; OMIM:600979
 A:Map position: 12p13.3-12p13.1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 10.1%; Score 251.5; DB 2; Length 435;
 Best Local Similarity 29.7%; Pred. No. 1.5e-09;
 Matches 106; Conservative 33; Mismatches 133; Indels 85; Gaps 22;

QY 2 GLSTVDDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVSGPGKTIHQNNSTCCT 60
 DB 11 GLAMGP---LVIGLFGLLAASQPOAV---PPYASENQTGRDQ---EKEYEPQHR-ICCS 60
 QY 61 KCHKGTYLVNDCPGPDPTDCRECSGFTASBNHRLHGLSCSKCKEMGOYEISCTVD 120
 DB 61 RCPDGYVNAKC-SRIRDVVCATCAENSTNEIMNYTLTQLCPDPPVGLIEIACIYK 119
 QY 121 RDTVCGCRNORYRHVWSENIPOCFNCISL--CLNGTVHLSCE--KONTVCT-CHAGFL 174
 DB 120 RTOCRQCPGMCAWA---LECTHCELLSDCPPTGEALKDBVKGNNHCYPCAKAGH- 175
 QY 175 RNEECVSCGNCKKSLSECTKLCI-POIENVKGTEDSGT-----VLL 214
 DB 176 -QNTSSPSARCPHTRCENQGL--VEADPTAOSDTCKNPLEPLRPENSGTMLAVLL 232
 QY 215 PLVIFGICLSLFLIGLMRYORWKS-----KIVSYVCGKSTPEKEGLEGTITKPLA 268
 DB 233 PLAFPL---LNAVTFSCI-----KSHPSLCRKLSGL--KRRQGES----- 270
 QY 269 PNP---SESPFPG--FTPLIGFSVPV-SSTFTSSSTYTPGDCPNFAAPREAVPYQ 319
 DB 271 PNPVAGSWEPKRAHRYFPLDVLPLISGDVSPVSGTLP-----AAPVLEAGVPOQ 321

RESULT 6
 GGHUN
 nerve growth factor receptor precursor, low affinity [validated] - human
 N:Alternate names: NGF receptor
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1998 #sequence_revision 31-Mar-1998 #text_change 08-Dec-2000
 C:Accession: A25218; A60204; S21689; J57638
 R:Johnson, D.; Lanhahn, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell,
 Cell 47, 545-554, 1986
 A:Title: Expression number and structure of the human NGF receptor.
 A:Reference number: A25218; MUID:87051725; PMID:3022937
 A:Accession: A25218
 A:Molecule type: mRNA
 A:Residues: 1-427 <JOH>
 A:Cross-references: GB:M14764; NID:9189204; PIDN:AA59544.1; PID:9189205
 R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob,
 J. Neurochem. 48, 225-232, 1987
 A:Title: Purification and amino terminal sequencing of human melanoma nerve growth fa
 A:Reference number: A60204; MUID:87085574; PMID:3023363
 A:Accession: A60204
 A:Molecule type: protein
 A:Residues: 29-31, 'T', '33-42', 'TT', '45-46', 'TX', '50-51', 'XX', '54-56 <MAR>
 A:Experimental source: melanoma cell line A875
 A:Note: this sequence has been corrected by a note added in proof to follow the nucle
 R:Visavajjalala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.


```

Db      246 RGTITD-----LIPYCSIIAAYVGLVATIAFRMNSCKOMKOGANRPVNGT----- 294
Qy      332 DPINPLQKWEDESAHKPOSILDTDDPAT-----LYAVV-----ENVPPL-- 369
Db      295 -PPEBEEKLHSDGISVDSGLHDQTHQTQTAGQALKGQGNLYSLPLTKREVERKLN 353
Qy      370 --RWKEFVRRLGLSDHEIDRLQLQNGRCLEAOYSMLATWRRTTPREATLEILGRVLRD 427
Db      354 GDTWIRIAGELGTQPEPHID--SFTHEACPVRA---LLASGADQ---SATLIDALLAALRR 405
Qy      428 MDLLGLELDEIEALC 442
Db      406 IQ-----RADIVESLC 416

```

RESULT 8

tumor necrosis factor receptor type 2 precursor - mouse

B38634

C.Species: Mus musculus (house mouse)

C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999

C.Accession: B38634; A40254; S54816

R.Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E. Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A.Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor

A.Reference number: A38634; MUID:91187885; PMID:1849278

A.Accession: B38634

A.Molecule type: mRNA

A.Residues: 1-474 <LEW>

A.Cross-references: GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828

R.Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk

Mol. Cell. Biol. 11, 3020-3026, 1991

A.Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A.Reference number: A40254; MUID:91246168; PMID:1645445

A.Accession: A40254

A.Molecule type: mRNA

A.Residues: 1-474 <GOO>

A.Cross-references: GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828

R.Kisomernighs, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.

Submitted to the EMBL Data Library, May 1995

A.Description: Characterization of the promoter region of the murine p75-TNF receptor.

A.Reference number: S54816

A.Accession: S54816

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-22 <RIS>

A.Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044

C.Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

C.Keywords: cytokine receptor; transmembrane protein

F.1-22/Domain: signal sequence #status predicted <SIG>

F.23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>

F.40-77/Domain: NGF receptor repeat homology <NGI>

F.79-120/Domain: NGF receptor repeat homology <NGI>

F.166-203/Domain: NGF receptor repeat homology <NGI>

Query Match 8.2%; Score 205; DB 2; Length 474;

Best Local Similarity 26.4%; Pred. No. 2.1e-06;

Matches 67; Conservative 30; Mismatches 105; Indels 52; Gaps 11;

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Qy      44 CPOGKTIHPONNSICTCKHKGTLYLNDPCPGQDTCRECSGFTASENHLRHCLSC- 102
Db      40 CQISQETVYRKAKMCCAKPQGYVKNFC-NKTSPTVCADCAASMTQYWNQFRCLSCS 98
Qy      103 SKCRKEMGOVEISSCTVDVDIVCGCRKNQY----RHYWSENLFQCFNCSLCLNG-TVHLS 157
Db      99 SSGCTVD--QVEIRACTKQONRVACACAGRYCALKTH--SGSCROCMRLSKCPCGCVASS 154
Qy      158 COEKONTVC-TCHAGFPLENEVCSCNCKSLECTKLCLEPIENVKG--TEDSGTIVLL 214
Db      155 RAPNGVNLCKACAPGTF--SDTTSSTDVCRPHRISIIAIPGNASTDAVCAPESTPLSAI 212
Qy      215 PLVIFPGICLLSLFLGLMYRYQRMKSKLYSVCGKSTPEKGELEGTTTKLAPNPSPS 274

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Db      213 PRTLYV-----SQPEP-----TRSQPLDQSPGPS 236
Qy      275 PTPGFTPLIGFSPV 288
Db      237 QPFSILTSLSGSTPI 250

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RESULT 9

148854

gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)

C.Species: Mus musculus (house mouse)

C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C.Accession: I48854

R.Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.

A.Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A.Reference number: I48854; MUID:95178848; PMID:7873884

A.Accession: I48854

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-459 <RES>

A.Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831

C.Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

F.151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 8.2%; Score 204.5; DB 2; Length 459;

Best Local Similarity 23.7%; Pred. No. 2.2e-06;

Matches 83; Conservative 43; Mismatches 145; Indels 79; Gaps 15;

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Qy      44 CPOGKTIHPONNSICTCKHKGTLYLNDPCPGQDTCRECSGFTASENHLRHCLSC- 102
Db      25 CQISQETVYRKAKMCCAKPQGYVKNFC-NKTSPTVCADCAASMTQYWNQFRCLSCS 83
Qy      103 SKCRKEMGOVEISSCTVDVDIVCGCRKNQY----RHYWSENLFQCFNCSLCLNG-TVHLS 157
Db      84 SSGCTVD--QVEIRACTKQONRVACACAGRYCALKTH--SGSCROCMRLSKCPCGCVASS 139
Qy      158 COEKONTVC-TCHAGFPLENEVCSCNCKSLECTKLCLEPIENVKG--TEDSGTIVLL 197
Db      140 RAPNGVNLCKACAPGTF--SDTTSSTDVCRPHRISIIAIPGNASTDAVCAPESTPLSAI 197
Qy      198 -----QIENVKGTEDS-----GTT-----VLPLVIFPGICLL 225
Db      198 PRTLYVQPEPRLPSQPLDQEPSPSTILVLSGSPPIEOSTKGCISLPIGLIVGVSLL 257
Qy      226 SLFLGIMTRYQRMKSKLYSVCGKSTPEKEGELGKTTKPLAPNPSPGFTPLIGF 285
Db      258 GILMLGIV-----NCFILVQRKKKPSG---LQRDADVPRHPDEKSGQDAVGLGQHLL 306
Qy      286 SVPVSTPFTS-SSVTPPGD--CPNPAAPREVAPPYGADPILATALASD 332
Db      307 TVAPSSSSSLESASAGDRRAPPGGHPQARVMAEAGSGQEARASSRISD 356

```

RESULT 10

GOVZML

T2 protein - myxoma virus (strain Lausanne)

C.Species: myxoma virus

C.Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999

C.Accession: A40566

R.Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.

Virolgy 184, 370-382, 1991

A.Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis

A.Reference number: A40566; MUID:91335768; PMID:1651597

A.Accession: A40566

A.Molecule type: DNA

A.Residues: 1-326 <UPN>

A.Cross-references: GB:M95181; GB:M37976; NID:9332309; PIDN:AAA46632.1; PID:9332310

C.Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

C.Keywords: glycoprotein

F.64-105/Domain: NGF receptor repeat homology <NG2>

F.106-147/Domain: NGF receptor repeat homology <NG3>

F.166,181,205,238/Binding site: carbohydrate (Asn) #status predicted

A:Molecule type: mRNA
 A:Residues: 1461 <END>
 A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA5929.1; PID:g189186
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.R.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring reference number: A36475; MUID:91045991; PMID:2172983
 A:Accession: A36475
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195, 'R', 197-461 <KOH>
 A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
 R:Dombi, C.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690; PMID:196549
 A:Accession: A48416
 A>Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AA19824.1; PID:g235649
 A:Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)
 R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of reference number: A36007; MUID:90349572; PMID:2166946
 A:Accession: A36007
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEU>
 A:Cross-references: GB:M35857; NID:g339751; PIDN:AA63262.1; PID:g339752
 R:Loetscher, H.; Schaefer, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors: A23666; MUID:91056048; PMID:2173696
 A:Accession: A23666
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-40/65-69/136-141/300-306 <LOB>
 R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence of reference number: A35010; MUID:90110215; PMID:2153136
 A:Accession: B35010
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R:Kühnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of A:Reference number: I38094; MUID:95121934; PMID:7821811
 A:Accession: I38094
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
 C:Genetics:
 A:Gene: GDB:TNR2
 A:Cross-references: GDB:125914; OMIM:191191
 A:Map position: 1p36.2-1p36.2
 A:Introns: 26/3
 A:Note: the list of introns is incomplete
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 F:1-22/Domain: duplication; glycoprotein; receptor; transmembrane protein
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG1>
 F:78-119/Domain: NGF receptor repeat homology <NG2>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>
 F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.4%; Score 183.5; DB 1; Length 461;
 Best Local Similarity 24.9%; Pred. No. 5,7e-05;
 Matches 72; Conservative 29; Mismatches 103; Indels 85; Gaps 14;
 42 SVPQGGKXIRPQNNSTICTCHNGTLYLNCPCGQOTDRECSGFTASENHLRCLS 101
 38 STCRRLREY-IDQTAQMCCKSCSPQGHAKVFCT-KTSPVCDSCSDSTYTQLMNVNPPCLS 95
 102 C-SKREKMGQVEISCTVDRTVCGCRKNQRYHWMSENLFQCPNCSICLNGTVHLSQCE 160
 96 CGSRCSDD--QVETQACTRQNRICTCRPG-----WICALSKQSCRLCA----- 138
 161 KQNTVCTCHAGFFL----RENECVSCSNC-----KSLSECTKICLP-QIENVKCTEDSGT 210
 139 ---PLRRCRPGFGVARRGTETSDVVCPCAPGTFESNTTSTDICRPHQICNV----- 187
 211 TVLLPLVIFPGCLSLFLIGLMRYQRMWSKLYICGKSTPEKEBELGCTTKPLAPN 270
 188 -VALP-----GNASMDAVCTSTSP-----TRSNAPG 212
 271 PSFSPTRPGFTPTLGSPVPS-STFTSSSTYP-----GDCPNFAP 310
 213 AVHLPPQVSTRSQHTQPTPEPSTAPSTSFLLPKPSPPAEGSTGDFALP 261

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 Job time : 23 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:07:00 ; Search time 36 Seconds
(without alignments)
2604.207 Million cell updates/sec

Title: US-09-899-429a-2

Perfect score: 2487
Sequence: 1 MGLSTVPDLPLPLVLELLV.....DIEEALCGPALPAPSLR 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_RHEM1.21:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriap:*
17: SP_Archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1801.5	72.4	446	6 Q95ND3	Q95ND3 felis silve
2	873	35.1	189	6 Q97530	Q97530 canis fami
3	866	34.8	189	6 Q95185	Q95185 felis silve
4	381.5	15.3	413	11 Q99MM1	Q99MM1 mus musculu
5	331	13.3	387	11 Q8VD70	Q8VD70 mus musculu
6	233	9.4	387	11 Q9PVD4	Q9PVD4 xenopus lae
7	230.5	9.3	433	11 Q912M6	Q912M6 rattus norv
8	227.5	9.1	368	13 Q57408	Q57408 melagris g
9	225	9.0	438	13 Q9DFV0	Q9DFV0 brachydanio
10	211	8.5	357	13 Q9DF34	Q9DF34 brachydanio
11	204.5	8.2	459	11 Q62327	Q62327 mus musculu
12	203.5	8.2	482	11 Q88734	Q88734 mus musculu
13	197	7.9	368	13 Q91AR7	Q91AR7 gallus gall
14	189.5	7.6	320	6 Q9XS29	Q9XS29 oryctolagus
15	189	7.6	319	6 Q9TV79	Q9TV79 oryctolagus
16	189	7.6	333	6 Q9BDP2	Q9BDP2 macaca mula

17	188	7.6	302	13 Q9PUS0	Q9PUS0 salveinus
18	188	7.6	331	6 Q9BDN0	Q9BDN0 macaca neme
19	187.5	7.5	334	6 Q9GL40	Q9GL40 macaca mula
20	187.5	7.5	651	13 Q98SM6	Q98SM6 gallus gall
21	187	7.5	368	13 Q9PW79	Q9PW79 gallus gall
22	186	7.5	331	6 Q9TSM4	Q9TSM4 macaca fasc
23	185.5	7.5	328	6 Q9BDP0	Q9BDP0 actus trivi
24	184	7.4	331	6 Q9GK36	Q9GK36 macaca assa
25	183.5	7.4	331	6 Q9BDN4	Q9BDN4 cercopithec
26	182.5	7.3	285	13 Q9DGH7	Q9DGH7 gallus gall
27	179	7.2	320	12 Q57079	Q57079 cowpox viru
28	179	7.2	322	12 Q72761	Q72761 cowpox viru
29	176.5	7.1	327	6 Q97491	Q97491 ovis aries
30	176	7.1	267	6 Q02764	Q02764 oryctolagus
31	176	7.1	277	6 Q8MMQ2	Q8MMQ2 ovis aries
32	176	7.1	283	6 Q9XS28	Q9XS28 cercopithec
33	175.5	7.1	312	13 Q9DGH8	Q9DGH8 gallus gall
34	174.5	7.0	320	12 Q57091	Q57091 ectromelia
35	174.5	7.0	320	12 Q57300	Q57300 ectromelia
36	174.5	7.0	347	12 Q57119	Q57119 cowpox viru
37	174	7.0	347	12 Q57115	Q57115 cowpox viru
38	174	7.0	350	12 Q57123	Q57123 cowpox viru
39	174	7.0	351	12 Q57121	Q57121 cowpox viru
40	173	7.0	401	13 Q9PRG7	Q9PRG7 xenopus lae
41	172.5	6.9	349	12 Q57100	Q57100 monkeypox v
42	172.5	6.9	360	12 Q57118	Q57118 cowpox viru
43	171.5	6.9	348	12 Q57092	Q57092 ectromelia
44	171.5	6.9	348	12 Q57277	Q57277 monkeypox v
45	171	6.9	326	12 Q57120	Q57120 cowpox viru

ALIGNMENTS

RESULT 1

ID: Q95ND3 PRELIMINARY; PRT: 446 AA.
AC Q95ND3;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Tumor necrosis factor type I.
GN TNFR I.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Goto Y., Baba K., Masuda K., Tsujimoto H.;
RT "Molecular cloning of feline tumor necrosis factor receptor type I
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in
RT cats";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051103; BAB55455.1; -;
DR InterPro: IPR000345; CYC_heme_bind.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS01166; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;

Query Match 72.4% Score 1801.5; DB 6; Length 446;
Best Local Similarity 75.8%; Pred. No. 1.1e-150;
Matches 348; Conservative 26; Mismatches 66; Indels 17; Gaps 8;

```

QY 1 MGLSTVPDLLPLVLLLELVGTPSGVIGLVPHLDREKRDSCVPGKXIIHPONNSICT 60
DB 1 MGLPTVGLDPLVLLALVETPLRVTLGRDLRDKRAALPCPGKXIIHPQDINSICT 60
QY 61 KCHKGTLYLNDGPGPQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGQVEISSCTVD 120
DB 61 KCHKGTLYLNDGPGPQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGQVEISSCTVD 120
QY 121 RDTVCCGRKNQRYHYWSENLFOCFNCSCLNGTVHLSCEQKONTVCTCHAGFFLRNECV 180
DB 121 RDTVCCGRKNQRYHYWSENLFOCFNCSCLNGTVHLSCEQKONTVCTCHAGFFLRNECV 180
QY 181 SCNCKKSLKCTICLPQLENNKGTEDSGTIVLPLVIFEGCLISLTGLMRYQRK 240
DB 181 SCVNCCKNCTKCLPVEIVKDPQDPTVLLPLVIFEGCLISLTGLMRYQRK 239
QY 241 SKLSTVCSKSTPEKEGEGTTPKPLAPNPSFPTPGTILGFSVPSTFSTSTT 300
DB 240 SKLSTVCSKSTPEKEGEGTTPKPLAPNPSFPTPGTILGFSVPSTFSTSTT 288
QY 301 PGDCPNE--AAPREYAPPYGADPILATASDPIPNFLQKWECSAH--KQSLDTDP 356
DB 289 PSDMANLRAASYREMAPPYGAGPILASAPASSPSTFVKQKEDSTHTQREDA--DPADP 347
QY 357 ATLVAVVENVPPLRKKEFRRLGSLSDHEDRLQNGRCLRAQYSMLATWRKRTPRRA 416
DB 348 ATLVAVVDVPPSRKKEFRRLGSLSEHERLELQNGRCLRAHYSMLAAMRRTPRRA 407
QY 417 TELLGRLVLRMDLGLCELDIEEALCGPALPPAPSLR 455
DB 408 TELLGRLVLRMDLGLCELDIEEALCAPASLSPAPRLR 446

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RESULT 2

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ID 097530 PRELIMINARY; PRT; 189 AA.
AC 097530;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor p60 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21109092; PubMed=11182158;
RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Dutchie S.,
RA Bennett D.;
RT "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL Vet. Immunol. Immunopathol. 78:207-214(2001).
DR EMBL; AF013955; AAD01516.1; -.
DR HSSP; P19438; 1TNR.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00505; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21324 MM; 5D3AD6A5676BFE99 CRC64;

```

Query Match

Best Local Similarity 35.1%; Score 873; DB 6; Length 189;
Matches 154; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

```

QY 1 MGLSTVPDLLPLVLLLELVGTPSGVIGLVPHLDREKRDSCVPGKXIIHPONNSICT 60
DB 1 MGLPTVGLDPLVLLALVETPLRVTLGRDLRDKRAALPCPGKXIIHPQDINSICT 60

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```

QY 61 KCHKGTLYLNDGPGPQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGQVEISSCTVD 120
DB 61 KCHKGTLYLNDGPGPQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGQVEISSCTVD 120
QY 121 RDTVCCGRKNQRYHYWSENLFOCFNCSCLNGTVHLSCEQKONTVCTCHAGFFLRNECV 180
DB 121 RDTVCCGRKNQRYHYWSENLFOCFNCSCLNGTVHLSCEQKONTVCTCHAGFFLRNECV 180
QY 181 SCNCKKSLKCTICLPQLENNKGTEDSGTIVLPLVIFEGCLISLTGLMRYQRK 240
DB 181 SCVNCCKNCTKCLPVEIVKDPQDPTVLLPLVIFEGCLISLTGLMRYQRK 239

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RESULT 3

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ID 095185 PRELIMINARY; PRT; 189 AA.
AC 095185;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor p60 (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC "Dutchie S., Nasir L., Eckersall P.D.;
RT "Felis catus" tumor necrosis factor receptor p60 (TNFR-1) mRNA,
RT partial cds.";
RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AB95089.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00505; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21420 MM; F3FBE0CE809D7DBE CRC64;

```

Query Match

Best Local Similarity 34.8%; Score 866; DB 6; Length 189;
Matches 155; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

```

QY 1 MGLSTVPDLLPLVLLLELVGTPSGVIGLVPHLDREKRDSCVPGKXIIHPONNSICT 60
DB 1 MGLPTVGLDPLVLLALVETPLRVTLGRDLRDKRAALPCPGKXIIHPQDINSICT 60
QY 61 KCHKGTLYLNDGPGPQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGQVEISSCTVD 120
DB 61 KCHKGTLYLNDGPGPQDTPDCRECSGSFTASENHLRHCLSCSKCKREMGQVEISSCTVD 120
QY 121 RDTVCCGRKNQRYHYWSENLFOCFNCSCLNGTVHLSCEQKONTVCTCHAGFFLRNECV 180
DB 121 RDTVCCGRKNQRYHYWSENLFOCFNCSCLNGTVHLSCEQKONTVCTCHAGFFLRNECV 180
QY 181 SCNCKKSLKCTICLPQLENNKGTEDSGTIVLPLVIFEGCLISLTGLMRYQRK 240
DB 181 SCVNCCKNCTKCLPVEIVKDPQDPTVLLPLVIFEGCLISLTGLMRYQRK 239

```

RESULT 4

Best Local Similarity 35.1%; Score 873; DB 6; Length 189;
Matches 154; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

```

ID 099MM1 PRELIMINARY; PRT; 413 AA.
AC 099MM1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

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DT 01-JUN-2002 (TEMBLrel. 21, last annotation update)
DE WSL-1-like protein.
GN TNFRSF12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA MEDLINE=21158384; Pubmed=11261933;
RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RA Owen M.J.,
RT "Genomic structure, expression, and chromosome mapping of the mouse
RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LAND, TR3, TNFRSF12)
RT gene."
RL Immunogenetics 53:59-63(2001).
DR EMBL: AF329969; AAK11256.1; .
DR HSP: P25943; 1CDP.
DR MCD: MGI:1934667; Tnftrsf12.
DR Interpro: IPR000488; Death.
DR Interpro: IPR000561; EGF-like.
DR Interpro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death.1.
DR Pfam: PF00020; TNFR_c6; 3.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00552; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 413 AA; 44453 MW; 69F21B85DDABAF CRC64;

Query Match 15.3%; Score 381.5; DB 11; Length 413;
Best Local Similarity 30.1%; Pred. No. 2.2e-25;
Matches 139; Conservative 53; Mismatches 176; Indels 91; Gaps 23;

QY 9 LLLPVLLELLVGIYPSGVTGLVPHLDREKRDSCVPOGKIYHPONNSICCTCKHKGTYL 68
DB 18 LLLLLLLLLLLGGGGGSGMGRCDASESQK-----YGPCCRCGCPKGYM 64
QY 69 YNDCPGPGDTCRCCESGSFTASENHLR-HCLSCSKCKEMGOYEISCTVDRPTVC 127
DB 65 KAPAEPCGNSTCLPCPSDFTLTRDNHFKTDCTRCQVCDERALQVTLNCSAKSDTHCGC 124
QY 128 RKNQRYHWSENLFCQENCSCLING-TVHLSG-----QEKONTVCTCHAGFELRENE 178
DB 125 QSG-----W-----CVDCSTVPCGKSSPSCVPCGATTPVHEAPTRPRCLPGFYINGND 173
QY 179 CVSG-----SNCKSLSECTKLCRPOIENVKGTEDS-GTVVLLPLVIFFGCLLSLFLIGL 232
DB 174 CTSCPTGFSVSCPKA--CTAVC-----GKMKFMVQVLLGVAFLGAILLIC----- 217
QY 233 MYRQHNKSKSYIVCGKSPKEKELEGGTTTKPLA-PNPSFPTPGFTPLIGSPVSS 291
DB 218 --AICRND-PCKAVV-----TADTAG-----TEPLASQTAHLASASASAPL-LAP-PS 262
QY 292 TFFSSST-----YTPGDCPNFAAPRREVAAPY-QGADPLATALASDPIPNLQWED 343
DB 263 TGCICTTIVOLGNMWTGISTQTEVVCQASQPMIDQLPNRTLGTRPLASPLSPAP----- 316
QY 344 SAHKPSLDDPATLYAAVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLREAOYSM 403
DB 317 PAFSPAIVLPGP-QLYDVMDAVPARMKKEFVRTLGREAIEAIVEICR-FRDOQYEM 374
QY 404 LATWRRTPRREATLELIGRLRMDLIGCLEDEIEAL 441
DB 375 LKRRQOP---AGLCAIYAALERKGLBGCAEDLRSL 409

AC Q8VD70;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 12.
GN TNFRSF12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC017526; AAI17526.1; .
DR MGI:1934667; Tnftrsf12.
DR Interpro: IPR000488; Death.
DR Interpro: IPR000561; EGF-like.
DR Interpro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR Pfam: PF00531; death.1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00552; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 387 AA; 41640 MW; F1664466BAD68D3 CRC64;

Query Match 13.3%; Score 331; DB 11; Length 387;
Best Local Similarity 27.9%; Pred. No. 5.8e-21;
Matches 127; Conservative 50; Mismatches 158; Indels 120; Gaps 21;

QY 9 LLLPVLLELLV--GIYPSGVTGLVPHLDREKRDSCVPOGKIYHPONNSICCTCKHKGTYL 66
DB 27 LLLPVLLELLVLLGGGGGSGMGRCDASESQK-----YGPCCRCGCPKGYM 73
QY 67 YLYNDCPGPGDTCRCCESGSFTASENHLR-HCLSCSKCKEMGOYEISCTVDRPTVC 125
DB 74 YMKAPCAEPCGNSTCLPCPSDFTLTRDNHFKTDCTRCQVCDERALQVTLNCSAKSDTHC 133
QY 126 GCRNQRYHWSENLFCQENCSCLINGTVHLSGCKEMGOYEISCTVDRPTVC 184
DB 134 CGQSG-----W-----CVDCSTVPCGKSSPSCVPCGATTPVHEAPTRPRCLPGFYINGND 173
QY 185 CKSLSECTKLCRPOIENVKGTEDSGTTVLL--PLVIFFGCLLSLFLIG--LMTRYQ 237
DB 147 PCGKSSPFS--CVP-----CGATTPVHEAPTRPRCLPGFYINGND 194
QY 238 RW-----KSKLIVCGKSTPEKELEGGTTTKPLA-PNPSFPTPGFTPLIGSPVSSFT 294
DB 195 RMQCKAVVADTAGTET-----LASPTAHLASASD-----ATL-LAP-PSSTGK 239
QY 295 SSSST-----YTPGDCPNFAAPRREVAAPY-QGADPLATALASDPIPNLQWEDSAH 346
DB 240 ICTTIVOLGNMWTGISTQTEVVCQASQPMIDQLPNRTLGTRPLASPLSPAP-----PAG 293
QY 347 KPSLDDPATLYAAVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLREAOYSMAT 406
DB 294 SPAIVLPGP-QLYDVMDAVPARMKKEFVRTLGREAIEAIVEICR-FRDOQYEM 374
QY 407 WRRTPRREATLELIGRLRMDLIGCLEDEIEAL 441
DB 352 WRQOP---AGLCAIYAALERKGLBGCAEDLRSL 383

RESULT 5
Q8VD70 PRELIMINARY; PRT; 387 AA.
ID Q8VD70

RESULT 6
Q9PVD4 PRELIMINARY; PRT; 387 AA.
ID Q9PVD4
AC Q9PVD4
DT 01-MAY-2000 (TEMBLrel. 13, Created)

DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE P75-1-like transmembrane protein fullback.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Hick E., Sun B.I., Collins-Racie L., Lavallie E., Sive H.L.;
 RT "Identification and Characterization of fullback, a Novel Posteriorly-
 RT Expressed Xenopus Gene";
 RT Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF131890; AAD34072.1; -;
 DR HSSP; P07174; INGR.
 DR InterPro: IPR001083; Copper-fist.
 DR InterPro: IPR004488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death_1.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR SMART; SM00412; Cu_FIST; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_3.
 DR PROSITE: PS50050; TNFR_NGFR_2; 4.
 DR Transmembrane.
 SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match 9.4%; Score 233; DB 13; Length 387;
 Best Local Similarity 22.6%; Pred. No. 2,6e-12;
 Matches 105; Conservative 63; Mismatches 166; Indels 130; Gaps 25;

QY 12 PVLLELVGIYPSGVIGLVPHLGREKRDVCPQGYIHPONNSICTCKCHKGYLYND 71
 DB 6 PVLTLCLL-----LISKISADYCESGLY--TNSKCCSLCPAGFCVVP 49
 QY 72 CCGPGDDTPCRRCC-ESGFTASENHLRHCLSCSKCKEMGOYEISCTYDRDTCGCRN 130
 DB 50 C--GSDTCEPCIENSTPSDVSAKAKCQPCFTCQSPSLTLE-SNCTREODTVCRCRPER 106
 QY 131 QYRHVSEMLFOCFNCSLCLNG-TVHLSQCEKONTVC-TCHAGFPLR---ENECVSC-S 183
 DB 107 QVLD--SNK--CLPCQLCSKGHGVISQCTHNKNYQQLCSSGFYSEVSSSPCLPCRT 162
 QY 184 NCKSELECTKLCLEPOLEINVKGTEDSGTIVLPLVIFGCLSLFLIGLMRYQRMKSKL 243
 DB 163 ECKETFEVQIGDCVPO----- 177
 QY 244 YSLVC-GKSTP---EKEGLEGTTRKPLAPNPSFSP---TPGFTPLLGSPVPSSTFTSS 296
 DB 178 HDILCDKDKVPLIKRTKEGENGST---AGSPHFIPODNSKNILPV--YCSIIAAVVGVL 231
 QY 297 STYTPGDCNFPAPRRREVAPRYOGADPILATFALASDPINPQKWD--SAHKPOSIDTD 354
 DB 232 IAYVAFKCTYTKQKKQAKARAGE---LATSTEGEKLINDSGVFIDTSLDPEPHLSK- 287
 QY 355 DPATLYAVE-----NVPLR-----WKEFYRRGLSDHEIDRLQLONG 393
 DB 288 -----AKTEPKLYINLPHKQSEVERLADTSLGDMQRLASLLGVEETIDTF-----G 337
 QY 394 RCLREKQYSMLATWRRTTRPRATTELLGRLVLRDMDLGLCLEDI 437
 DB 338 RG-EDPVHLLTDW---SSKESSTLEVLCALVNMERADVENTL 377

RESULT 7
 ID 0912M6 PRELIMINARY; PRT; 433 AA.
 AC 0912M6;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, last sequence update)

DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
 DE Tumor necrosis factor receptor type II (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
 RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
 RT capillary endothelial cells and participate in TNF-alpha transport
 RT through the blood-brain barrier";
 RL Submitted (Sep-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF420214; AAL16021.1; -;
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 DR Receptor.
 KW Receptor.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 433 AA; 45723 MW; 7573D835E72CA4A CRC64;

Query Match 9.3%; Score 230.5; DB 11; Length 433;
 Best Local Similarity 24.7%; Pred. No. 4,9e-12;
 Matches 91; Conservative 46; Mismatches 152; Indels 79; Gaps 16;

QY 24 PSGVIGLVPHLDREKRDVCPQGYIHPONNSICTCKCHKGYLYNDGPGDPCRE 83
 DB 4 PAKYV-LTRY---KRPNGQCQISQGYIDKKAQMCCKAPPGQYAKHFC-NKTSPTVCAD 58
 QY 84 CEGSFTASENHLRHCLSC-SKCRKEMGOYEISCTYDRDTCGCRKNQY--RHYWSENL 140
 DB 59 CAAGMETQVWNHLRHCLSCSSSCSD--QVETHNCTKNQRYCACNADSYCALKLSGNC 116
 QY 141 FCFNCSLCLNG-TVHLSQCEKONTVC-TCHAGFPLREKVCSCSKCKSLCTKLCPL- 197
 DB 117 RCKMKLSKGPFGVARSFTSNGNVYCSACAPGT--STTSSTVDCRPHRCSILAIPTG 174
 QY 198 -----QIENVGTEDS-----GTT----- 211
 DB 175 NASTDAVCASESPSPAVRITVYSPETRSQPMQDEGSPQTHIPVLSGSTPIERS 234
 QY 212 ----VLPLVIFFGCLSLFLIGLMRYQRMKSKYISVCGSKSPKEGELGTTKPL 267
 DB 235 ITGGISLPIGLIVGLTTLGLMLGL-----ANCFILVQKKRPPSC--LQRETMVPH 283
 QY 268 APNPSFTPTPTPLGSPVPSSTFTS-SSTYTPGD--CPNPAAPRRVAPPYGADPI 324
 DB 284 LPDEKSDQAVGLEQHLTTTAPSSSSSSLESSASAGDRRAPPGVAPQARVTAAGSDEA 343
 QY 325 LATALASD 332
 DB 344 CAGSRSSD 351

RESULT 8
 ID 057408 PRELIMINARY; PRT; 368 AA.
 AC 057408;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE Subgroup E AlV receptor.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OC NCBI_TaxID=9103;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97471016; PubMed=9326659;
 RA Adkins H.B., Brojatsch J., Naughton J., Rolis M.M., Resola J.M.,

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RA Young J.A.;
RT "Identification of a cellular receptor for subgroup E avian leukosis
  virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622(1997).
DR EMBL: AF006002; AB93987.1; -.
DR HSSP: 014763; 1D0G.
DR InterPro: IPR001450; 4Fe4S_ferredoxin.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001865; Ribosomal_S2.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KM Receptor.
SQ SEQUENCE 368 AA; 41020 MW; 5701AC2A6DAF87E2 CRC64;

Query Match          9.1%; Score 227.5; DB 13; Length 368;
Best Local Similarity 23.8%; Pred. No. 7.4e-12;
Matches 107; Conservative 46; Mismatches 172; Indels 125; Gaps 19;

OY 14 VLLELVGTPSGVIGLVPHLGDRKRDVCPGQKYIHPONNSICTCHKGTLYNDGP 73
DB 11 VLLLLALKV-----HLGSAAVAKRAVKSDVLKPDPS--KKCPGTYLAND-- 55
OY 74 GPGDDTCRCEESGFTASENHLRHCLSCSKCKEMQOVELISCTVDRODYCCGRKNOR 133
DB 56 ----SSKCLPKCKDEYETPRDPKCLGCRTRCD--QVEVSPCNSTRNTRCKACK----- 104
OY 134 HYWSENFQCFNCSLCINGVHLSQCKOKMTVCTCHAGFLENECVSCSNCK----- 186
DB 105 -----NGT-----FCLPDHPCEMCQCKQCRKPGQ 129
OY 187 -KSLSECK---LCLEPQIENVKGTEDSGTYV--LLPLVIFEGCLLSLFT-----G 231
DB 130 VIRACQOOSDLRCGPPLDSSSFTTGIIISTVLPVLLVLLCCCCCRYSASGG 189
OY 232 LMYVQRMKSLYSIVCGKSPKEKEGEGTTTKPLAPNPFSPTPPTPLTGFSPSS 291
DB 190 VLSKRPAMAKILL-----QRMGIQDNNCNQIYQOQOQOQOQLITTEQG--SEVPRG 240
OY 292 TETSSSTYTPGDCPNFAAPRRVAPPYOGADPILATALASDPIPNPLQKWDASHKPSQ 351
DB 241 VEVEVEEVAP--RTPNVEIQRLV--PYPGKDP--TVLSS-----SF 277
OY 352 DTDDPATLYAVENVPLRMKEFYVRLGLSDHEIDRLQLONGRCLREAOYSMLATWRRT 411
DB 278 NT-----FVDLPVPRQMRFRGALGLRENNLYQAE-QNDRSGEPLYMLIMLMKE 328
OY 412 PRREATLELGRVLRMDLGLCELDIEAL 441
DB 329 GSK-ASVNTLLETLSQISLGSVADIASEL 357

RESULT 9
O9DFV0 PRELIMINARY; PRT; 438 AA.
AC O9DFV0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ovarian TNF receptor.
CN TNFRSF8A.
OS Brachydanio rerio (Zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;

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RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
  RT ligands in the fish ovary.";
RL EMBL: AF250042; AAC24365.1; -.
DR HSSP: 014763; 1D0G.
DR ZFIN: ZDB-GENE-010802-1; tnfrsf8a.
DR InterPro: IPR000345; Cyt_c_heme_bld.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 3.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KM Receptor.
SQ SEQUENCE 438 AA; 49103 MW; B7E5312BE6E80B04 CRC64;

Query Match          9.0%; Score 225; DB 13; Length 438;
Best Local Similarity 21.7%; Pred. No. 1.5e-11;
Matches 111; Conservative 53; Mismatches 170; Indels 178; Gaps 24;

OY 1 MGLSTVPDLPLVLELVGTPSGVIGLVPHLGDRKRDVCPGQ-KYIHPONNSICC 59
DB 1 MDKSEAMKVCMAVLIYFSLALVGHGAELGVSADQNQNTARQMTLENHNEYH---NPFCC 57
OY 60 TKCHKGTLYNDGCPGDDTCRCEESGFTASENHLRHCLSCSKCKEMQOVELISCTV 119
DB 58 KNCAGTYVKEKCYSGHYMGKSCPEKGTVAEHTGTGHEQCICQCHRDQ----- 107
OY 120 DROTVCCGRKNQYHYWSENFQCFNCSLCINGVHLSQCKOKMTVCTCHAGFLENE 178
DB 108 -----TVVABCTYSTMTKCDCKFGTCLDDEP 134
OY 179 ---CVSCNCKSLSECKRLCP-----QLENVGTEDESGTT-VLLPLVI 218
DB 135 CEVCKKCTKCKADEEVEVSGCPTSNTRKRRRPSVPTGPPRKPSASNSTGIIYIVGLI 194
OY 219 FPGICLL--SLPTGLMRYQRMKS-----KLYSIYCGKSTPEKEG----- 257
DB 195 LTVICTIVGAILF--LKRROQOSETNGNLEEVKVPIDECPRSEEGQENRNAGLEKEE 251
OY 258 -----ELEGTTK-----PLAPNPSPSP--GTPPT 282
DB 252 EHPRESAPLLTQETQETGSKSIPVEDEDRGIGDSLPHNQLFPRKPSLSALPQNHMGFT-- 309
OY 283 LGFSVPVSSSTFTSSSTYTPGDCPNFAAPRRVAPPY-OGADPILATALASDPIPN--PL 336
DB 310 --VDPAP-----RPRDRPT-----EIRLNHGKRD-----DP-PRKLLPL 341
OY 339 QKWEDSAHKPSQSLDTPDPATLYAVENVPLRW-KEFYVRLGLSDHEIDRLQLONGRCL 397
DB 342 LGEEESLSK--SFDLFDLSL-----DVRYHNKFRFSIGVSDNSIKLAETQOP--M 386
OY 398 EAQYSMLATWRRTPRREATLELGRVLRMD 429
DB 387 DKVYDLRWVMMQKEGLR-ANINTLLQALDLD 417

RESULT 10
O9DF34 PRELIMINARY; PRT; 357 AA.
AC O9DF34;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Death receptor.
OS Brachydanio rerio (Zebrafish) (zebra danio).

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QY 9 LLLPLVLELLVGVISGVIGLYPHLGDRKRDVCPQGIYIHONNSICTCKHKTYL 68
DB 6 VLLPLI-LTICIAG-----SLSTINDCKIKNETQYSTGL--SGNFCCOLCPPTKK 54
QY 69 YNDPCPGQDTPDCRECSGSGFTASENHLRHCLSCSKCRKEMGOVEISSCTVDRDTCGR 128
DB 55 KACDTSNEKRPDCEPCEGEEYTDKSHF-----SSKCR----- 88
QY 129 KNOYRHYWSENLFQCFNCISCLNG---TVHLSQCKONTVCTCHAGFF--LRENECVS 181
DB 89 -----CSIC-DGEHGLEVEITDCTTIQNTKCKCKSNFNCNALKECHCDP 130
QY 182 CSNCKKSL--ECTKLCIPQIENVKGTEDSGTVLLPLVIFPGICLSLFTIGL-MRYOR 238
DB 131 CTMCEHGIIECT-----QTSNCKCKEKGSTTSKHHFWL-LCILLIPVIGLRKXK 184
QY 239 WSKLTSIVCGKSTPEKEGELEGTTRKPLAPNPSFPTPGFTPLGSPVPSSTFTSSST 298
DB 185 HRD-----GKHGYDK----- 194
QY 299 YTPGDCPNFAAPRREVAAPYOGADPILATLASDPILPNLQKWDNSAHKPOSLDTPDPAT 358
DB 195 -----STALIEGVPMNFS-----DVDISKY 215
QY 359 YAVVENVPPLRMKEFYRRLGSLDHEIDRLQLONGRCLREAOYSMLATWRRRTPREATL 418
DB 216 IPTAEEMKINEVEKFRKNGVNEAKIDEIKNDIQTAEQVOLLRNWHQLHGKRDAYNT 275
QY 419 ELGRVLRDMDLGLCLEDIEE 439
DB 276 LTI-KGIRKANLCAIAEKIOD 295

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RESULT 15
Q9TV79 PRELIMINARY; PRT; 319 AA.

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ID 09TV79
AC 09TV79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE B-type Fas antigen.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Isono T., Tanabe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB021298; BAA78430.1; -.
DR HSSP: P25443; 1DDF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death. 1.
DR Pfam: PF00020; TNFR_c6; 3.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 319 AA; 35961 MW; 06FA0033B1846591 CRC64;

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Query Match 7.6%; Score 189; DB 6; Length 319;
Best Local Similarity 19.8%; Pred. No. 1.6e-08;
Matches 87; Conservative 53; Mismatches 140; Indels 160; Gaps 15;

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QY 9 LLLPLVLELLVGVISGVIGLYPHLGDRKRDVCPQGIYIHONNSICTCKHKTYL 68
DB 6 VLLPLI-LTICIAG-----SLSTINDCKIKNETQYSTGL--SGNFCCOLCPPTKK 54
QY 69 YNDPCPGQDTPDCRECSGSGFTASENHLRHCLSCSKCRKEMGOVEISSCTVDRDTCGR 128
DB 55 KACDTSNEKRPDCEPCEGEEYTDKSHF-----SSKCR----- 88
QY 129 KNOYRHYWSENLFQCFNCISCLNG---TVHLSQCKONTVCTCHAGFF--LRENECVS 181
DB 89 -----CSIC-DGEHGLEVEITDCTTIQNTKCKCKSNFNCNALKECHCDP 130
QY 182 CSNCKKSL--ECTKLCIPQIENVKGTEDSGTVLLPLVIFPGICLSLFTIGL-MRYOR 238
DB 131 CTMCEHGIIECT-----QTSNCKCKEKGSTTSKHHFWL-LCILLIPVIGLRKXK 184
QY 239 WSKLTSIVCGKSTPEKEGELEGTTRKPLAPNPSFPTPGFTPLGSPVPSSTFTSSST 298
DB 185 HRD-----GKHGYDK----- 194
QY 299 YTPGDCPNFAAPRREVAAPYOGADPILATLASDPILPNLQKWDNSAHKPOSLDTPDPAT 358
DB 195 -----STALIEGVPMNFS-----DVDISKY 215
QY 359 YAVVENVPPLRMKEFYRRLGSLDHEIDRLQLONGRCLREAOYSMLATWRRRTPREATL 418
DB 216 IPTAEEMKINEVEKFRKNGVNEAKIDEIKNDIQTAEQVOLLRNWHQLHGKRDAYNT 275
QY 419 ELGRVLRDMDLGLCLEDIEE 439
DB 276 LTI-KGIRKANLCAIAEKIOD 295

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DB 55 KACDTSNEKRPDCEPCEGEEYTDKSHF-----SSKCR----- 88
QY 129 KNOYRHYWSENLFQCFNCISCLNG---TVHLSQCKONTVCTCHAGFF--LRENECVS 181
DB 89 -----CSIC-DGEHGLEVEITDCTTIQNTKCKCKSNFNCNALKECHCDP 130
QY 182 CSNCKKSL--ECTKLCIPQIENVKGTEDSGTVLLPLVIFPGICLSLFTIGL-MRYOR 239
DB 131 CTMCEHGIIECT-----QTSNCKCKEKGSTTSKHHFWL-LCILLIPVIGLRKXK 184
QY 240 KSLTSIVCGKSTPEKEGELEGTTRKPLAPNPSFPTPGFTPLGSPVPSSTFTSSST 299
DB 185 RD-----GKHGYDK----- 193
QY 300 TPGDCPNFAAPRREVAAPYOGADPILATLASDPILPNLQKWDNSAHKPOSLDTPDPATL 359
DB 194 -----STALIEGVPMNFS-----DVDISKY 215
QY 360 YAVVENVPPLRMKEFYRRLGSLDHEIDRLQLONGRCLREAOYSMLATWRRRTPREATL 419
DB 216 PTIAEEMKINEVEKFRKNGVNEAKIDEIKNDIQTAEQVOLLRNWHQLHGKRDAYNT 275
QY 420 ILGRVLRDMDLGLCLEDIEE 439
DB 276 LTI-KGIRKANLCAIAEKIOD 294

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Search completed: December 27, 2002, 15:09:46
Job time : 38 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2002, 19:14:10 ; Search time 65 Seconds
(without alignments)
8206.584 Million cell updates/sec

Title: US-09-899-429A-1
Perfect score: 1368
Sequence: 1 atgggcctctccacgcgtgc.....cgccagctcttcagatga 1368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEM_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	100.0	1368	9	US-09-898-234-1
2	1368	100.0	1368	9	US-09-899-429A-1
3	1368	100.0	1368	10	US-09-899-422-1
4	1368	100.0	2141	9	US-09-898-234-16
5	1368	100.0	2141	9	US-09-899-429A-26
6	1368	100.0	2141	10	US-09-899-422-16
7	1366.4	99.9	2111	10	US-09-880-107-2360
8	1366.4	99.9	2175	12	US-10-130-397-1
9	1122	82.0	1334	9	US-09-898-234-11
10	1122	82.0	1334	10	US-09-899-422-11
11	1117.2	81.7	1334	9	US-09-899-429A-21
12	743.4	54.3	2130	10	US-09-917-800A-1601
13	735.4	53.8	2173	9	US-09-898-234-14
14	735.4	53.8	2173	9	US-09-899-429A-24
15	735.4	53.8	2173	10	US-09-899-422-14
16	685.4	50.1	2440	10	US-09-970-532-1
17	633	46.3	633	9	US-09-899-429A-7
18	603	44.1	603	9	US-09-899-429A-13
19	557	40.7	600	9	US-09-899-429A-11

20	546	39.9	549	9	US-09-899-429A-9	Sequence 9, Appl1
21	527	38.5	570	9	US-09-899-429A-17	Sequence 17, Appl1
22	516	37.7	519	9	US-09-899-429A-15	Sequence 15, Appl1
23	514	37.6	1301	10	US-09-756-186-7	Sequence 7, Appl1
24	513	37.5	516	9	US-09-899-429A-19	Sequence 19, Appl1
25	506	37.0	1147	10	US-09-756-186-5	Sequence 5, Appl1
26	483	35.3	483	9	US-09-898-234-3	Sequence 3, Appl1
27	483	35.3	483	9	US-09-899-429A-3	Sequence 3, Appl1
28	483	35.3	483	10	US-09-899-422-3	Sequence 3, Appl1
29	483	35.3	483	10	US-09-907-263-1	Sequence 1, Appl1
30	483	35.3	486	9	US-09-899-429A-5	Sequence 5, Appl1
31	424.4	31.0	1049	10	US-09-756-186-1	Sequence 1, Appl1
32	424.4	31.0	1202	10	US-09-756-186-3	Sequence 3, Appl1
33	337	24.6	427	10	US-09-876-589-236	Sequence 236, App
34	330	24.1	543	10	US-09-970-532-3	Sequence 3, Appl1
35	329.6	24.1	5870	10	US-09-838-718A-8	Sequence 8, Appl1
36	140.4	10.3	158	9	US-09-898-234-66	Sequence 68, Appl1
37	140.4	10.3	158	9	US-09-899-422-68	Sequence 68, Appl1
38	134	9.8	158	9	US-09-899-429A-78	Sequence 78, Appl1
39	124.4	9.1	413	10	US-09-960-352-2885	Sequence 2885, Ap
40	123.2	9.0	151	9	US-09-898-234-20	Sequence 20, Appl1
41	123.2	9.0	151	9	US-09-899-429A-30	Sequence 30, Appl1
42	123.2	9.0	151	10	US-09-899-422-20	Sequence 20, Appl1
43	98.2	7.2	154	10	US-09-783-590-8601	Sequence 8601, Ap
44	87	6.4	87	9	US-09-898-234-5	Sequence 5, Appl1
45	87	6.4	87	10	US-09-899-422-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-898-234-1
Sequence 1, Application US/09898234
Patent No. US2002015112A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Haumer, Adolph
APPLICANT: Mauser-Fogy, Ingrid
APPLICANT: Stralowa, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
FILE REFERENCE: 98,385-I
CURRENT APPLICATION NUMBER: US/09/898,234
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/525,998
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1368
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1368)
NAME/KEY: sig_peptide
LOCATION: (1)..(87)
NAME/KEY: misc_feature
LOCATION: (88)..(120)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion.
NAME/KEY: misc_feature
LOCATION: (606)..(633)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by

OY	1	ATGGCCCTCTCACCGGCGCGAGACCTCTCTCGACACTGGTGCTCTGGAGCGTTGGTG	60
Db	1	ATGGCCCTCTCACCGGCGCGAGACCTCTCTCGACACTGGTGCTCTGGAGCGTTGGTG	60
OY	61	GGAAATATACCCCTCAGGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGA	120
Db	61	GGAAATATACCCCTCAGGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAAGA	120
OY	121	GATAGTGTGTCTCCCAAGGAAAATATATCCACCCTCAAAATATATTCGATTGTGTAC	180
Db	121	GATAGTGTGTCTCCCAAGGAAAATATATCCACCCTCAAAATATATTCGATTGTGTAC	180
OY	181	AAGTGCACCAAGGAACTACTATTACATAGACGTACAGGCGCCGGGGAGATACGGAC	240
Db	181	AAGTGCACCAAGGAACTACTATTACATAGACGTACAGGCGCCGGGGAGATACGGAC	240
OY	241	TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACTCAGACACTGCC	300
Db	241	TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACTCAGACACTGCC	300
OY	301	AGCTGTCTCAAAATCCCAAAAGGAATGGTTCAGGTGAGATCTCTTTCGACAGTGAC	360
Db	301	AGCTGTCTCAAAATCCCAAAAGGAATGGTTCAGGTGAGATCTCTTTCGACAGTGAC	360
OY	361	CGGGACACCGGTGTGGCTGAGGAAGAACATACCGGATATATGGGTGAAAACTT	420
Db	361	CGGGACACCGGTGTGGCTGAGGAAGAACATACCGGATATATGGGTGAAAACTT	420
OY	421	TTCCAGTGTCTCAATTCACGCTCTGCGCTCAATAGGAGACGTGCACCTCTCGCCAGAG	480
Db	421	TTCCAGTGTCTCAATTCACGCTCTGCGCTCAATAGGAGACGTGCACCTCTCGCCAGAG	480
OY	481	AAACAGAACACCGTGTGCACCTGCGCATGCAGGTTCTTCTTAAGAAAAAGATGTGTG	540
Db	481	AAACAGAACACCGTGTGCACCTGCGCATGCAGGTTCTTCTTAAGAAAAAGATGTGTG	540
OY	541	TTCGTGTGTACTGTAGAAAAAGCGTGGATGACGAAATGTGTGCTTACCCAGATTGAG	600
Db	541	TTCGTGTGTACTGTAGAAAAAGCGTGGATGACGAAATGTGTGCTTACCCAGATTGAG	600
OY	601	AATGTTAAGGCACTGAGGACTCAGGACACACAGTCTGTGGCCCTGTCTCATTTTCTTT	660
Db	601	AATGTTAAGGCACTGAGGACTCAGGACACACAGTCTGTGGCCCTGTCTCATTTTCTTT	660
OY	661	GGCTTTGCCCTTTTATCCCTCTCTTCATTGGTTAATGATCGTACCAAGGTTGAG	720
Db	661	GGCTTTGCCCTTTTATCCCTCTCTTCATTGGTTAATGATCGTACCAAGGTTGAG	720
OY	721	TCCCAAGCTACTACCATTTGTTGTGGGAAATGCACACCTGAAAAAGAGGGGAGCTTGA	780
Db	721	TCCCAAGCTACTACCATTTGTTGTGGGAAATGCACACCTGAAAAAGAGGGGAGCTTGA	780
OY	781	GGAACTACTACTAAGCCCTGTGGCCCAAAACCAAGCTCAGTACGCCCTCAGAGCTTAC	840
Db	781	GGAACTACTACTAAGCCCTGTGGCCCAAAACCAAGCTCAGTACGCCCTCAGAGCTTAC	840
OY	841	CCGACCTGGGCTTCACTGCCGTGCCAGTTCACACTTCACGCTCAGCTACACTATAC	900
Db	841	CCGACCTGGGCTTCACTGCCGTGCCAGTTCACACTTCACGCTCAGCTACACTATAC	900
OY	901	CCGCGTGTACTGTCCCAACTTGGCGGCTCCCGGAGAGAGTGGACACACTTATAGGGG	960
Db	901	CCGCGTGTACTGTCCCAACTTGGCGGCTCCCGGAGAGAGTGGACACACTTATAGGGG	960
OY	961	GCTACCCCAATCTTGTGGAGAGCCCTTGCCCTCCGACCCCATCCCAACCCCTTGAAG	1020
Db	961	GCTACCCCAATCTTGTGGAGAGCCCTTGCCCTCCGACCCCATCCCAACCCCTTGAAG	1020
OY	1021	TGGAGAGACAGCGCCCAAGCCACAGAGCTTAGACATGATGACCCCGCGAGCGCTGAC	1080
Db	1021	TGGAGAGACAGCGCCCAAGCCACAGAGCTTAGACATGATGACCCCGCGAGCGCTGAC	1080

QY	1081	GGCGTGTGTAAGACGTGCCCCCGTGTGCGTGAAGAAATTCGTGGCGGCGCTAGAGGCTG	1140
DB	1081	GGCGTGTGTAAGACGTGCCCCCGTGTGCGTGAAGAAATTCGTGGCGGCGCTAGAGGCTG	1140
QY	1141	AGCGACCCAGAGATGCATGCGCTGGAGCTGCAGAACGCGCGCTGCTCGCGAGCGCA	1200
DB	1141	AGCGACCCAGAGATGCATGCGCTGGAGCTGCAGAACGCGCGCTGCTCGCGAGCGCA	1200
QY	1201	TTCACAGATGCTGGACCTGGAGCGGGCGACACGCGCGGCGGAGGCGCACGGCTGAGCGT	1260
DB	1201	TTCACAGATGCTGGACCTGGAGCGGGCGACACGCGCGGCGGAGGCGCACGGCTGAGCGT	1260
QY	1261	CTGGGACGGGTGCTCCGCGACATGAGACCTGCTGGGCTGCTGGAGACATCGAGAGCGG	1320
DB	1261	CTGGGACGGGTGCTCCGCGACATGAGACCTGCTGGGCTGCTGGAGACATCGAGAGCGG	1320
QY	1321	CTTTGCGGCGCCCGCGCCCTCCCGCGCGCCAGTCTTCTCAGATGA	1368
DB	1321	CTTTGCGGCGCCCGCGCCCTCCCGCGCGCCAGTCTTCTCAGATGA	1368
RESULT 4			
US-09-898-234-16			
Sequence 16, Application US/09898234			
Patent No. US20020155112A1			
GENERAL INFORMATION:			
APPLICANT: Hauptmann, Rudolph			
APPLICANT: Himmeler, Adolph			
APPLICANT: Maurer-Fogy, Ingrid			
APPLICANT: Stralowa, Christian			
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for			
TITLE OF INVENTION: Them			
FILE REFERENCE: 98,385-I			
CURRENT APPLICATION NUMBER: US/09/898,234			
CURRENT FILING DATE: 2001-07-03			
PRIOR APPLICATION NUMBER: 09/525,998			
PRIOR FILING DATE: 2000-03-15			
PRIOR APPLICATION NUMBER: 08/383,676			
PRIOR FILING DATE: 1995-02-01			
PRIOR APPLICATION NUMBER: 08/153,287			
PRIOR FILING DATE: 1993-11-17			
PRIOR APPLICATION NUMBER: 07/821,750			
PRIOR FILING DATE: 1992-01-02			
PRIOR APPLICATION NUMBER: 07/511,430			
PRIOR FILING DATE: 1990-04-20			
NUMBER OF SEQ ID NOS: 87			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 16			
LENGTH: 2141			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (213)..(1580)			
OTHER INFORMATION: Description of Artificial Sequence: human TNF-R 1n			
OTHER INFORMATION: 1TNF-R2			
US-09-898-234-16			
Query Match			
Best Local Similarity 100.0%; Score 1368; DB 9; Length 2141;			
Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGGCTCTCCACCGCTGACCTGCTGCTGCGCCACTGGTGTCTCTCTGAGCTGTGGTG	60
DB	213	ATGGGCTCTCCACCGCTGACCTGCTGCTGCGCCACTGGTGTCTCTCTGAGCTGTGGTG	272
QY	61	GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCCTCAGCTAGGGGACAGGGAAGAGA	120
DB	273	GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCCTCAGCTAGGGGACAGGGAAGAGA	332
QY	121	GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATATATTCGATTGTGTAC	180
DB	333	GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATATATTCGATTGTGTAC	392

181 AAGTCCCAAGGAGACCTACTTGTACAAATGACHTCCAGGCCGCGGGGACAGATACGGAC 240
393 AAGTGCCCAAGGAGACCTACTTGTACAAATGACHTCCAGGCCGCGGGGACAGATACGGAC 452
241 TGCAGGAGAGTGTAGAGACGCGCTCTTCACCGCTTCAGAAAACCACTCAGACACTGCTC 300
453 TGCAGGAGAGTGTAGAGAGGCGCTCTTCACCGCTTCAGAAAACCACTCAGACACTGCTC 512
301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 360
513 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 572
361 CGGAGACACCGGTGTGGTGTGAGGAAGAACAGTACCGGCAATTTGAGTGAAGAAACCTT 420
573 CGGAGACACCGGTGTGGTGTGAGGAAGAACAGTACCGGCAATTTGAGTGAAGAAACCTT 632
421 TTCCAGTGTCTCAATTTGACAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 480
633 TTCCAGTGTCTCAATTTGACAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 692
481 AAACGAAACACCGGTGTGACAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 540
693 AAACGAAACACCGGTGTGACAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 752
541 TTCTGTAGTACTGTGAAGAAAAGCTGGAGTGCAGGAAAGTGTGCTTACCCCAATTTGAG 600
753 TTCTGTAGTACTGTGAAGAAAAGCTGGAGTGCAGGAAAGTGTGCTTACCCCAATTTGAG 812
601 AATGTAAAGGACACTGAGAGACTCAGAGCACACAGTGTGTTGCCCTGATTTCTTT 660
813 AATGTAAAGGACACTGAGAGACTCAGAGCACACAGTGTGTTGCCCTGATTTCTTT 872
661 GGTCTTTGGCTTTTATCCCTCTCTTCAATGTTTAAATGATGCTTACCAAGGTGAG 720
873 GGTCTTTGGCTTTTATCCCTCTCTTCAATGTTTAAATGATGCTTACCAAGGTGAG 932
721 TCCAAAGCTCTGATCATTTGTTGTTGGGAAATGACACCTGAAAGAAAGGGGAGCTTGA 780
933 TCCAAAGCTCTGATCATTTGTTGTTGGGAAATGACACCTGAAAGAAAGGGGAGCTTGA 992
781 GGAACACTACTAAGCCCTGCGCCCAAAACCAAGCTTCACTTCCACTCAGGCTTCAAC 840
993 GGAACACTACTAAGCCCTGCGCCCAAAACCAAGCTTCACTTCCACTCAGGCTTCAAC 1052
841 CCAACCTGCGGCTTCAAGTCCCGTCCAGTTCACCTTCACTTCCAGCTTCACTTAC 900
1053 CCAACCTGCGGCTTCAAGTCCCGTCCAGTTCACCTTCACTTCCAGCTTCACTTAC 1112
901 CCGGTGACCTGTCCCAACTTTGGGCTCCCGGACAGAGAGTGGGACCCCTATCAGGG 960
1113 CCGGTGACCTGTCCCAACTTTGGGCTCCCGGACAGAGAGTGGGACCCCTATCAGGG 1172
961 GCTGACCCCATCTTTGGGACAGCCCTGCTTCGACCCCATCCCAACCCCTTACAGAG 1020
1173 GCTGACCCCATCTTTGGGACAGCCCTGCTTCGACCCCATCCCAACCCCTTACAGAG 1232
1021 TGGGAGACAGCGCCGACAGCCACAGAGCTTACACTGATGACCCCGGACAGCTGTAC 1080
1233 TGGGAGACAGCGCCGACAGCCACAGAGCTTACACTGATGACCCCGGACAGCTGTAC 1292
1081 GCGGTGAGAGAGTGTGCGGCTGGGCTGGGAAAGAAATGCGTGGGCGGCTAGGGCTG 1140
1293 GCGGTGAGAGAGTGTGCGGCTGGGCTGGGAAAGAAATGCGTGGGCGGCTAGGGCTG 1352
1141 AGCGACACAGAGATGATCGGTGAGCTGAGAAACGGGCGCTGCTCGGAGGCGCAA 1200
1353 AGCGACACAGAGATGATCGGTGAGCTGAGAAACGGGCGCTGCTCGGAGGCGCAA 1412
1201 TACAGCATGCTGGGAGCTTGAAGGCGGCGACGCGGCGGCGGAGGCGACGCTGAGCTG 1260
1413 TACAGCATGCTGGGAGCTTGAAGGCGGCGACGCGGCGGCGGAGGCGACGCTGAGCTG 1472

1261 CTGGAGCGCGTCTCCGCGACATGAGACTGTGGCTGCTGCTGAGAGCATGAGAGGCG 1320
1473 CTGGAGCGCGTCTCCGCGACATGAGACTGTGGCTGCTGCTGAGAGCATGAGAGGCG 1352
1321 CTTTGGCGCGCGCGCGCGCTCCCGCGCGCGCCAGTCTTCTCAGATGA 1368
1533 CTTTGGCGCGCGCGCGCGCTCCCGCGCGCGCCAGTCTTCTCAGATGA 1580

RESULT 5
US-09-899-429a-26
; Sequence 26, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hammler, Adolph
; APPLICANT: Maurer-Fogly, Ingrid
; APPLICANT: Stralowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2141
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R 1n
; OTHER INFORMATION: LTNF-R2
; NAME/KEY: CDS
; LOCATION: (213)..(1577)
US-09-899-429a-26

Query Match 100.0%; Score 1368; DB 9; Length 2141;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGGCTCTCTCCACCGTGCCTGACCTGTGCTGCTGACAGTGTGCTCTGAGACTGTGGTG 60
213 ATGGGCTCTCTCCACCGTGCCTGACCTGTGCTGCTGACAGTGTGCTGAGACTGTGGTG 272
61 GGAATATACCCCTCAGAGGCTATTGAGCTGTCCCTCAGCTTACAGGAGGAGGAGAGAGA 120
273 GGAATATACCCCTCAGAGGCTATTGAGCTGTCCCTCAGCTTACAGGAGGAGGAGAGAGA 332
121 GATAGTGTGTGTCCCAAGGAAATATATTCACCTCAAAATTAATTCATTGGCTGATGAC 180
333 GATAGTGTGTGTCCCAAGGAAATATATTCACCTCAAAATTAATTCATTGGCTGATGAC 392
181 AAGTGCCCAAGGAGACCTACTTGTACAAATGACHTCCAGGCCGCGGGGACAGATACGGAC 240
393 AAGTGCCCAAGGAGACCTACTTGTACAAATGACHTCCAGGCCGCGGGGACAGATACGGAC 452
241 TGCAGGAGAGTGTAGAGAGGCGCTCTTCACCGCTTCAGAAAACCACTCAGACACTGCTC 300
453 TGCAGGAGAGTGTAGAGAGGCGCTCTTCACCGCTTCAGAAAACCACTCAGACACTGCTC 512
301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 360


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Db 693 AAACAGAACACCGTGTGCACCTGCATGCAAGTTCTTCTAAGAAAAACAGGTGTGC 752
Qy 541 TCCTGTAGTACTGTAAAGAAAAAGCTGGAGTGCAGAAATTGTGCTACCCAGATGAG 600
Db 753 TCCTGTAGTACTGTAAAGAAAAAGCTGGAGTGCAGAAATTGTGCTACCCAGATGAG 812
Qy 601 AATGTTAAGGGACGTAGAGACTCAGGCACACAGTGTGCTTGTGCTTGTCAATTTCTTT 660
Db 813 AATGTTAAGGGACGTAGAGACTCAGGCACACAGTGTGCTTGTGCTTGTCAATTTCTTT 872
Qy 661 GGTCTTTGGCTTTTATCCCTCTCTCATTTGTTTAAATGATGCTTACCAAGGTTGAAG 720
Db 873 GGTCTTTGGCTTTTATCCCTCTCTCATTTGTTTAAATGATGCTTACCAAGGTTGAAG 932
Qy 721 TCCAACTTACTCCATTGTTTGTGGGAAATGACACCTGAAAAAGAGGGAGCTTGA 780
Db 933 TCCAACTTACTCCATTGTTTGTGGGAAATGACACCTGAAAAAGAGGGAGCTTGA 992
Qy 781 GGAACACTACTAAGGACCCCTGGGCCCCAAACCAAGCTTGAATGCCACTGCAGGCTTAC 840
Db 993 GGAACACTACTAAGGACCCCTGGGCCCCAAACCAAGCTTGAATGCCACTGCAGGCTTAC 1052
Qy 841 CCCACCCCTGGGCTTCAGTCCGTCGCCAGTTCACCTTCACCTCCAGCTTCACTTATAC 900
Db 1053 CCCACCCCTGGGCTTCAGTCCGTCGCCAGTTCACCTTCACCTCCAGCTTCACTTATAC 1112
Qy 901 CCCGCTGACTGTCCCAACTTTGGGCTCCCGCCAGAGAGTGGCACACCTATACAGGG 960
Db 1113 CCCGCTGACTGTCCCAACTTTGGGCTCCCGCCAGAGAGTGGCACACCTATACAGGG 1172
Qy 961 GGTGACCCCATCTCTGCGACAGGCTCGCTCGACCCCATCCCAACCCCTTCGAAG 1020
Db 1173 GGTGACCCCATCTCTGCGACAGGCTCGCTCGACCCCATCCCAACCCCTTCGAAG 1232
Qy 1021 TGGGAGACAGGCGCCACAAAGCCACAGACCTAGACATGATGACCCCGCGAGCTGTAC 1080
Db 1233 TGGGAGACAGGCGCCACAAAGCCACAGACCTAGACATGATGACCCCGCGAGCTGTAC 1292
Qy 1081 GCCGTGTGTGAGAACTGCCCCCGTGTGCGCTGGAAAGAAATTCGTGGGCGCTTACAGG 1140
Db 1293 GCCGTGTGTGAGAACTGCCCCCGTGTGCGCTGGAAAGAAATTCGTGGGCGCTTACAGG 1352
Qy 1141 ACGGACACAGAGATGATGGCTGAGCTGCGAAGACGGGCGCTGCTGGCGAGGCGCAA 1200
Db 1353 ACGGACACAGAGATGATGGCTGAGCTGCGAAGACGGGCGCTGCTGGCGAGGCGCAA 1412
Qy 1201 TACAGCATCTGGCGACCTGAGAGCGCGCACGCGCGCGGCGAGGCGCAAGCTGAGCTG 1260
Db 1413 TACAGCATCTGGCGACCTGAGAGCGCGCACGCGCGCGGCGAGGCGCAAGCTGAGCTG 1472
Qy 1261 CTGGGACCGGTGCTCCGCGACATGACCTGCTGGGCTGCTGGAGCAATCGAGAGCGG 1320
Db 1473 CTGGGACCGGTGCTCCGCGACATGACCTGCTGGGCTGCTGGAGCAATCGAGAGCGG 1532
Qy 1321 CTTTGGGCGCGCGCGCTCCCGCGCGGCGCGAGTCTCTCAGATGA 1368
Db 1533 CTTTGGGCGCGCGCGCTCCCGCGCGGCGCGAGTCTCTCAGATGA 1580

RESULT 7
US-09-880-107-2360
; Sequence 2360, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-MO
; CURRENT APPLICATION NUMBER: US/09/880.107
; CURRENT FILING DATE: 2001-06-14
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; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2360
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M58286
US-09-880-107-2360

Query Match          99.9%  Score 1366.4  DB 10:  Length 2111:
Best Local Similarity 99.9%  Pred. No. 0:
Matches 1367; Conserved 0; Mismatches 1; Indels 0; Gaps 0:

Qy 1 ATGGGCGCTCCACCGCTGCTGACCTGCTGCGCCACTGTGCTCCTGGAGCTGTGGTG 60
Db 187 ATGGGCGCTCCACCGCTGCTGACCTGCTGCGCCACTGTGCTCCTGGAGCTGTGGTG 246
Qy 61 GGAATATACCCCTCAGAGGGTTATTGACGTGTCCTTACCTAAGGGACAGAGAGAGA 120
Db 247 GGAATATACCCCTCAGAGGGTTATTGACGTGTCCTTACCTAAGGGACAGAGAGAGA 306
Qy 121 GATAGTGTGTCCCAAGGAAATATATCCACCCTCAAAATATATTCGATTGCTTACC 180
Db 307 GATAGTGTGTCCCAAGGAAATATATCCACCCTCAAAATATATTCGATTGCTTACC 366
Qy 181 AATGCGCAAAAGGAAGTACTTGTACAAATGACTGTCCAGGCGCGGCGAGATACGAG 240
Db 367 AATGCGCAAAAGGAAGTACTTGTACAAATGACTGTCCAGGCGCGGCGAGATACGAG 426
Qy 241 TGCAGGAGTGTGAGAGCGGCTTCACCGCTTCAGAAAACCACTCAGACACTGCTTC 300
Db 427 TGCAGGAGTGTGAGAGCGGCTTCACCGCTTCAGAAAACCACTCAGACACTGCTTC 486
Qy 301 AGCTGCTCCAAATCCGAAAGGAAATGGTCAAGGTGAGATCTCTTGTGCACAGTGCAC 360
Db 487 AGCTGCTCCAAATCCGAAAGGAAATGGTCAAGGTGAGATCTCTTGTGCACAGTGCAC 546
Qy 361 CGGAGACCGGTGTGCTGACAGGAAACAGTACCGGCATTTATGGAGTGAACCTT 420
Db 547 CGGAGACCGGTGTGCTGACAGGAAACAGTACCGGCATTTATGGAGTGAACCTT 606
Qy 421 TTCAGTGTCTCAATTTGACGCTCTGCTCAATGGAGACCGTGCACCTCTCTCCAGAG 480
Db 607 TTCAGTGTCTCAATTTGACGCTCTGCTCAATGGAGACCGTGCACCTCTCTCCAGAG 666
Qy 481 AAACAGAACACGCTGTGACCTGTCCATGCAAGTTTCTTCTAAGAAAAACGAGTGTTC 540
Db 667 AAACAGAACACGCTGTGACCTGTCCATGCAAGTTTCTTCTAAGAAAAACGAGTGTTC 726
Qy 541 TCCTGTAGTACTGTAAAGAAAAAGCTGAGTGCAGCAAGTTGTGCTTACCCAGATGAG 600
Db 727 TCCTGTAGTACTGTAAAGAAAAAGCTGAGTGCAGCAAGTTGTGCTTACCCAGATGAG 786
Qy 601 AATGTTAAGGGACGTAGAGACTCAGGCACACAGTGTGCTTGTGCTTGTCAATTTCTTT 660
Db 787 AATGTTAAGGGACGTAGAGACTCAGGCACACAGTGTGCTTGTGCTTGTCAATTTCTTT 846
Qy 661 GGTCTTTGGCTTTTATCCCTCTCTCATTTGTTTAAATGATGCTTACCAAGGTTGAAG 720
Db 847 GGTCTTTGGCTTTTATCCCTCTCTCATTTGTTTAAATGATGCTTACCAAGGTTGAAG 906
Qy 721 TCCAACTTACTCCATTGTTTGTGGGAAATGACACCTGAAAAAGAGGGAGCTTGA 780
Db 907 TCCAACTTACTCCATTGTTTGTGGGAAATGACACCTGAAAAAGAGGGAGCTTGA 966
Qy 781 GGAACACTACTAAGGACCCCTGGGCCCCAAACCAAGCTTGAATGCCACTGCAGGCTTAC 840
Db 967 GGAACACTACTAAGGACCCCTGGGCCCCAAACCAAGCTTGAATGCCACTGCAGGCTTAC 1026
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[illegible]

RESULT 8
US-10-120-397-1
Sequence 1, Application US/10120397
Patent No. US20020142357A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BRAEBROSCCH, Cord
TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/120,397
FILING DATE: 12-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/054,970
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

[illegible]

Db 365 GATAATTTGTGTCCCGAGGAAAGTATGCCATCCAAAGAAATATTCATCTGTGCAC 424
Oy 181 AAGTGCACAAAGAAACCTACTGTATGATGATGATCCAGGCCCGGGGAGGATPAGGAC 240
Db 425 AAGTGCACAAAGAAAGAACTACTGTGTGATGATGATCCAGGCCCGGGGAGGAAACAGTC 484
Oy 241 TGCAGGAGGTGTGAGAGGGCTCTTTCACCCGCTCAGAAACACCTCAGACATGCTC 300
Db 485 TGCAGAGCTCTCTCATTAAGAGGACCTTTACAGCTTGCAGAAACACAGTGCAGAGTGTCTC 544
Oy 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGGAGATCTCTTTCAGACAGTGAC 360
Db 545 AGTTCAGAGACATGTGTGGGAAAGAAATGTTCACAGTGGAGATTTCTTCTGCAACCTGAC 604
Oy 361 CGGGACACCGTGTGTGGCTGCAGAAAGAAACGATCCGCGCATTTTGGAGTAAACCTT 420
Db 605 ATGACACACCGTGTGTGGCTGCAGAAAGAAACCAATTCACAGCTACCTGTGATGAGCGAT 664
Oy 421 TTCCAGTGTCTCAATTTGACAGCTCTGCTCAATGGGACCGCTCACCTCTCTGCCAGAG 480
Db 665 TTCCAGTGTGTGACTGCAGAGCCCTGCTTCAATGGGACCGCTGACATCCCTGTAAAGAG 724
Oy 481 AAACAGAACACCGTGTGCACCTGCATGCAGGTCTTCTTAAGAAAGAAACGATGTCTC 540
Db 725 AAACAGAACACCGTGTGTAACTGTACGACGAGGATTTCTTCTAAGCGAAATGATGCAC 784
Oy 541 TCCCTAGTAAGTAAAGAAAGCCTGGAGTGCAGAGATTTGCTTACCCAGATGAG 600
Db 785 CTTTCAGCAGCTGCAGAAAGAAATCAGAAATATGATGATGATGCTTACCTCAGTGTGA 844
Oy 601 AATGTTAAGGACATGAGAGCTCAGGACACAGATGCTTGGCCCTGCTATTTCTTT 660
Db 845 AATGTCACAAACCCGAGGACACAGGATCTGCGGTGTGTCTGTCTGTATCTTCTTA 904
Oy 661 GGTCTTTGCTTTTATTCCTCTCTCTTCAATGGTTAATGATATGCTACCAAGTGAAG 720
Db 905 GGTCTTTGCTTTTATTTCTTATCTGACATCACTGATGCTGCGATATCCCAAGTGAAG 964
Oy 721 TCCAAAGCTCTACTCATTTGTTGGGAAATGACACCTGAAAGAGGAGGAGCTTGA 780
Db 965 CCCAGGCTCTACTCATTTGTTGGGATGATGATGATGATGATGATGATGATGATGAT 1024
Oy 781 GGAAGTACTACTAGCCCT 834
Db 1025 GGAATTTGTTACTAAGCCCTTACTGACAGCTCTATGCCAGCTTACGCCCAACCCGCGC 1084
Oy 835 TTACACCCCAACCTGAGGCTTCACTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 879
Db 1085 TTCAACCCCAACCTGAGGCTTCACTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1144
Oy 880 ACCCTCAGCTCAGCTATATACCCCGGTGACGTGCCAACTTGGCGCTCCCGCAGAGAG 939
Db 1145 CCCATCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
Oy 940 GTGACACCAACCTTATCAGGAGGCTGACCCCATCTTGCACAGCCCTGCTGCTGCTGCTG 999
Db 1205 GTGGTGTCCAAAC---CAGGCTGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1261
Oy 1000 ATCCCAACCCCTTTCAGAGTGGAGAG---CAGGCTCACAAGCCACAGACCTGAC 1056
Db 1262 ATCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
Oy 1057 ACTGATGACCCCGGACGCTGTACGCGGTGGAGAAAGTGTCCCGCTGGGCTGGAGAG 1116
Db 1322 ACTGACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1381
Oy 1117 GATTTCTGTGCGGCTTAAAGCTGAGCGACACAGATGATGCTGCTGCTGCTGCTGCTGCT 1176
Db 1382 GAGTTCTATGCGGCTCTCTGCGGCTGAGCGACAGATGAGACGGTGTGAAGTGTGCTGCT 1441
Oy 1177 GGGCGCTGCTGCTGCGGAGGCGCAATACAGATGCTGCGACCTGGAGGCGGCGACGCGG 1236
Db 1442 GGGCGCTGCTGCTGCGGAGGCTCATTAAGCATGCTGGAAGCCTGGGCGGCGGACACCGG 1501

Oy 1237 CGGCGAGGCGCCAGCTGAGCTGCGGAGCGCTGCTCCGACATGAGCTGTGGGC 1296
Db 1502 CGACACAGGCGCCAGCTGAGCTAGTGGCGCGCTGCTTGTGGACATGAACTGCTGGC 1561
Oy 1297 TGCCTGAGAGACATGAGAGGCGCTTGGCGCCCGCC 1335
Db 1562 TGCCTGAGAGACATCGCGGAGACTCTAGAAACCCCTGCC 1600
RESULT 14
US-09-899-429a-24
; Sequence 24, Application US/09899429A
; Patent No. US20020169118A1
GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurel-Fogy, Ingrid
; APPLICANT: Stralowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899, 429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477, 639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383, 676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 24
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ratTNF-R8
; NAME/KEY: CDS
; LOCATION: (245)..(1627)
US-09-899-429a-24
Query Match 53.8%; Score 735.4; DB 9; Length 2173;
Best Local Similarity 73.7%; Pred. No.1.le-177;
Matches 1001; Conservative 0; Mismatches 331; Indels 27; Gaps 4;
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Db 245 AAGGCGCTCTCCACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
Oy 61 GGAATATACCCCTCAGAGGCTTATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 305 GGAATATACCCCTCAGAGGCTTATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
Oy 121 GATAGTGTGTGCCCAAGAAATATATACACCCCTCAAAATATATGATTTGCTGTAC 180
Db 365 GATATTTTGTGTGCCCAAGAAATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
Oy 181 AAGTGCACAAAGAAACCTACTTGTATCAATGACTGTCCAGGCCCGGCGGAGATACGAC 240
Db 425 AAGTGCACAAAGAAACCTACTTGTGAGTGTGACTGTCCAAAGCCAGGCGAGAAACAGTC 484
Oy 241 TGCAGGAGTGTGAGAGCGCTCTTACACCGCTTACAGAAACCACTCTGACAGATGCTC 300
Db 485 TGCAGAGCTCTCTATTAAGAGCACTTTTACAGCTTGTCCAAACCACTCTGACAGATGCTCTC 544
Oy 301 ACTGCTCCAAATGCCGAAAGAAATGGGTCAAGTGGAGATCTCTTCTTGCACAGTGTAC 360

Db 725 AAMCAGAACCCGTGTGTAACGTGCCACGAGATTCTTCTAAGCGAAATGATGCACC 784
Oy 541 TCCGTGTAAGTGTAAAGAAAAGCCTGGAGTGTGCAGAAAGTGTGCTACCCAGATTGAG 600
Db 785 CTTTCAGACCCTGCAAGAAAATGAGAAATGATGAAGCTGTGCTACCTCCAGTTGCA 844
Oy 601 AATGTTAAGGGCACTGAGAGACTCAGGACACAGAGTGTGTCCTGCTGTCATTTTCTTT 660
Db 845 AATGTCACAAACCCAGAGACTCAGAGTACTGCGGCTGTGCCCTGTGTTATCTTCCTA 904
Oy 661 GGTCTTTCCTTTTATTCCTCTCTTCATTTGTTTAAATGATGCTTACCAAGGTGAAG 720
Db 905 GGTCTTTCCTTTTATTTCTTTATCTGATCAAGTCACTGTGCCGATATCCCAAGTGAAG 964
Oy 721 TCCAGCTCTACTCCATGTTGTGGAAATGCACCTGAAAAAGAGGGAGCTTGA 780
Db 965 CCCAGGCTACTCATTTGATGGAATTCAGCTCTGTCMAAGAGGTGAGGGTGA 1024
Oy 781 GGAACCTACTACTAAGCCCT-----GGCCCAACCCAGGCTTCAGTCCCACTCCAGG 834
Db 1025 GGAATTGTTACTAAGCCCTTAAGCTCAGCTTATCCAGCTTCAGCCCAACCCCGGC 1084
Oy 835 TTGACCCCGACCCGTGGCTTCAGTCCGTCGCCAG-----TTCACCTTC 879
Db 1085 TTCAACCCCACTGTGGCTTCAGCACACCCAGCCTTCAGTCACTGTCTCCAGTACC 1144
Oy 880 ACCTCAGACTCAGCTATACCCCGGTGACTGTCCCACTTGGCGCTCCCGCAGAGAG 939
Db 1145 CCCATCAGCCCGCTGTGCTGCTAGTAACTGGCACAACTTCGTGCTCACCTGTGAAGAG 1204
Oy 940 GTGCAACACCCCTATCAGGGGGGTGACCCCACTTGGCACAGCCCTGCGCTCCGACCC 999
Db 1205 GTGGTCCCAAC---CAGGGTCTGACCTCTCTCTAGGATCCCTCAACCTGTGCCA 1261
Oy 1050 ATCCCAACCCCTTCAGAAAGTGGAGGA---CAGCGCCCAACAGCACAGAGCCTAGAC 1056
Db 1262 ATCCCGCCCTGTTCGGAATGGGAAGCGTCTGCGGGCCAGCACAAACGGCTTGAC 1321
Oy 1057 ACTGATGACCCCGGAGCCTGTACCGCGTGGTGAAGAGTGCCTGCGCTGGAG 1116
Db 1322 ACTGAGACCCCTGCTGATGCTGTGATGCTGTGATGGCTGCTCGACACGCTGGAAG 1381
Oy 1117 GAATTGCTGCGCGGCTAGGAGCGACGACGATCGATCGGCTGGAGCTGCAGAAC 1176
Db 1382 GAGTTCATGCGGCTCTCTGGGCTGAGCGACGACGATCGAGCGTTGGAGCTGCAGAAC 1441
Oy 1177 GGGCGCTGCTGCGGAGGCGCAATACAGCATGTGGCGACCTGGAGGCGGCGCACGCG 1236
Db 1442 GGGCGTTGGCTCGGGAGGCTCATTAACAGCATGTGGAAGCCTGGCGGGCGCGCACCG 1501
Oy 1237 CGGCGGAGGCGCAGCTGAGCTGCTGGAGCGGTGCTCCGACATGAGCCTGCTGGGC 1296
Db 1502 CGACACGAGGCGCACGCTGAGCTAGTGGGCCGCTGCTTTGCGACATGAACCTGCGTGC 1561
Oy 1297 TGCCGTGAGGAGCATGAGAGGCGCTTGGCGGCCCGCC 1335
Db 1562 TGCCGTGAGAGCATCGCGAGACTCTAGAAAGCCCTGCC 1600

Search completed: December 4, 2002, 20:15:47
Job time : 99 secs

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GenCore version 5.1.3
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Om nucleic - nucleic search, using sw model

Run on: December 4, 2002, 19:14:50 ; Search time 265 Seconds
(without alignments)
11625.410 Million cell updates/sec

Title: US-09-899-429A-1
 Perfect score: 1368
 Sequence: 1 atgggcctctcacgltgcc.....cgccagctcttcagatga 1368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

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24:	/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1366.4	99.9	1368	14	AA049932	Lambda-derived TNF
2	1366.4	99.9	1368	21	AA95105	Human TNFR1 coding
3	1366.4	99.9	2088	12	AA010883	30X3 TNF inhibitor
4	1366.4	99.9	2088	22	AA083846	Human 30 kDa TNF 1
5	1366.4	99.9	2111	20	AA209170	Human tumor necro
6	1366.4	99.9	2111	22	AAH48859	Human TNFRP-associ
7	1366.4	99.9	2111	24	ABK94039	Human CDNA differe
8	1366.4	99.9	2111	24	ABN95862	Gene #2360 used to
9	1366.4	99.9	2161	21	AA248475	Human tumor necro

10	1366.4	99.9	2161	24	ABK131954	Human tumour necro
11	1364.8	99.8	2111	12	AAO109555	Encodes human 55kD
12	1364.8	99.8	2175	16	AAO90513	p55 TNF-R gene. H
13	1363.2	99.6	2062	13	AAO20973	TNF-alpha binding
14	1363.2	99.6	2062	13	AAO24440	Encodes TNF-alpha
15	1361.6	99.5	2176	12	AAO12215	Type I TNF receptor
16	1361.6	99.5	2141	11	AAO06285	Human Tumour Necro
17	1360	99.4	2170	14	AAO050870	p55 Tumour necrosi
18	1120.4	81.9	1334	11	AAO06282	Plasmid Tumour Necr
19	743.4	54.3	2130	24	ABK63694	Rat Sequence diffe
20	732.2	53.5	2173	18	AAO06284	Rat Tumour Necrosi
21	632.8	46.3	1926	11	AAV00431	Vector pCDNA3-19G1
22	632.4	46.2	6889	17	AAV15931	DHFR/Intinon (WTas
23	596.8	43.6	608	13	AAO24441	Encodes truncated
24	515.4	37.7	1478	20	AAK58150	Cdc4-fusion polyep
25	514	37.6	1301	18	AAV94022	CDNA for TBP(20-19
26	506	37.0	1147	18	AAV94021	CDNA for TBP(20-19
27	501.4	36.7	504	13	AAO24445	Encodes truncated
28	483	35.3	483	19	AAV15448	Human soluble tumo
29	483	35.3	483	19	AAV19801	Soluble tumour necr
30	483	35.3	483	20	AAV81732	Tumour necrosis in
31	483	35.3	483	22	AAK83945	Human 30 kDa TNF-1
32	440	32.2	2254	21	AAV95107	Partial human TNFR
33	424.4	31.0	1049	18	AAV94007	CDNA for TBP(20-16
34	424.4	31.0	1202	18	AAV94008	CDNA for TBP(20-16
35	418	30.6	1674	21	AAZ50196	Male fusion plasmid
36	381	27.9	1977	24	ABA99913	TNF-selectokine pr
37	376.2	27.5	477	13	AAO24444	Encodes truncated
38	375.8	27.5	507	24	ABL99490	Tagged canine gene
39	357.2	26.1	474	13	AAO24442	Encodes truncated
40	329.6	24.1	5870	21	AAAI15044	Nucleotide sequenc
41	312.4	22.8	339	19	AAV19804	Truncated sTNFR, s
42	310.8	22.7	462	13	AAO24443	Encodes truncated
43	308.2	22.5	333	19	AAV19805	Truncated sTNFR, s
44	304.4	22.3	332	19	AAV18803	Truncated sTNFR, s
45	294.6	21.5	315	19	AAV18806	Truncated sTNFR, s

ALIGNMENTS

ID	AAQ49932	standard; CDNA to mRNA; 1368 BP.
AC	AAQ49932;	
DT	29-APR-1994	(first entry)
XX	Lambda-derived TNF-R cDNA.	
XX	Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;	
KW	IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;	
KW	rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;	
KW	pulmonary fibrosis; silicosis; allograft; xenograft; rejection;	
KW	grat versus host disease; sepsis; inflammation; allergy;	
KW	autoimmune dysfunction; ss.	
OS	Homo sapiens.	
OS	Lambda-gt10-7-ctnbp.	
PH	Key	Location/Qualifiers
FT	CDS	1..1366
FT		/*tag= a
FT		/product= hTNF-R
FT	sig_peptide	1..120
FT		/*tag= b
FT	mat_peptide	121..1363
FT		/*tag= c
XX	WO9319777-A.	
XX		
PD	14-OCT-1993.	

DE	Human TNFR1 coding sequence.
XX	
KW	TNFR1; tumour necrosis factor receptor; polymorphism; human;
KW	tumour; cancer; apoptosis; bacterial infection; ds.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
FT	1..1368
FT	/*tag= a
FT	/product= "TNFR1"
FT	1..39
FT	/*tag= b
FT	/number= 1
FT	replace(36,G)
FT	/*tag= c
FT	40..193
FT	/*tag= d
FT	/number= 2
FT	194..322
FT	/*tag= e
FT	/number= 3
FT	replace(224,T)
FT	/*tag= f
FT	replace(269,T)
FT	/*tag= g
FT	323..472
FT	/*tag= h
FT	/number= 4
FT	replace(362,A)
FT	/*tag= i
FT	replace(403,C)
FT	/*tag= j
FT	473..551
FT	/*tag= k
FT	/number= 5
FT	552..625
FT	/*tag= l
FT	/number= 6
FT	626..739
FT	/*tag= m
FT	/number= 7
FT	740..768
FT	/*tag= n
FT	/number= 8
FT	769..1057
FT	/*tag= o
FT	/number= 9
FT	1058..1368
FT	/*tag= p
FT	/number= 10
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PN	WO20050436-A1.
XX	
PD	31-AUG-2000.
XX	
PE	23-FEB-2000; 2000WO-US04606.
XX	
PR	23-FEB-1999; 99US-0121314.
XX	
PA	(GENA-) GENAISSANCE PHARM INC.
PA	(NAND/) NANDABALAN K.
PA	(SCHU/) SCHULZ V P.
PA	(STEP/) STEPHENS J C.
PA	(CHEW/) CHEW A.
XX	
PI	Nandabalan K, Schulz VP, Stephens JC, Chew A;
XX	
DR	WPI: 2000-543909/49.
DR	P-PSDB: AAB23446.
XX	
PT	Polynucleotides comprising polymorphic variants of a reference sequence for tumour necrosis factor receptor 1 (TNFR1), useful for studying the

Query Match	Best Local Similarity	Score	DB	Length
Matches 1367; Conservative	99.9%; Pred. No. 0;	1366.4;	21;	1368;
	0; Mismatches	1;	Indels	0; Gaps
				0;
1	ATGGGCTCTCCACCGTCCGACCTGCTGCACTGGTGGTGGTGGG	60		
1	ATGGGCTCTCCACCGTCCGACCTGCTGCACTGGTGGTGGTGGG	60		
61	GGAATATCCCTCAGGGGTTATGGACGTGGTCCCTCAGGAGGAGAGAGA	120		
61	GGAATATCCCTCAGGGGTTATGGACGTGGTCCCTCAGGAGGAGAGAGA	120		
121	GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATATTCGATTTGCTGTACC	180		
121	GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATATTCGATTTGCTGTACC	180		
181	AAATGCCCAAAAGAACCTACTTGTACAAATGACTGTCCAGGCGCGGAGATACGAC	240		
181	AAATGCCCAAAAGAACCTACTTGTACAAATGACTGTCCAGGCGCGGAGATACGAC	240		
241	TGCAGGGGTGTGAGAGGGGCTCCTCACCGCTTCAAAAACACGTCAGACCTGCCAC	300		
241	TGCAGGGGTGTGAGAGGGGCTCCTCACCGCTTCAAAAACACGTCAGACCTGCCAC	300		
301	AGCTGCTCAAAATGCGCAAGAAATGGTACAGTGGAGATCTCTTTCGACAGTGGAC	360		
301	AGCTGCTCAAAATGCGCAAGAAATGGTACAGTGGAGATCTCTTTCGACAGTGGAC	360		
361	CGGACACCGTGTGTGCTGCGAGAGAACCACTACCGGCAATTTTGGAGTAAACCTT	420		
361	CGGACACCGTGTGTGCTGCGAGAGAACCACTACCGGCAATTTTGGAGTAAACCTT	420		
421	TTCCAGTCTTCATATGAGCGCTGTGCTCAATGGGACCGTGGACCTCTTCGCGAGAG	480		
421	TTCCAGTCTTCATATGAGCGCTGTGCTCAATGGGACCGTGGACCTCTTCGCGAGAG	480		
481	AAACAGAACACCGTGTGCTGCACTGCAATGACAGTCTCTTAAAGAGAAAACGAGTGTGC	540		
481	AAACAGAACACCGTGTGCTGCACTGCAATGACAGTCTCTTAAAGAGAAAACGAGTGTGC	540		
541	TCCTGTAGTAACTGTAAAGAAAAGCCTGAGTGCACGAAGTTGGCTTACCCAGATTGAG	600		
541	TCCTGTAGTAACTGTAAAGAAAAGCCTGAGTGCACGAAGTTGGCTTACCCAGATTGAG	600		
601	AATGTTAAGGGCAGTGAAGAGTCAAGGACCAACATGCTGTGGCCCTGGGCAATTTCTTT	660		
601	AATGTTAAGGGCAGTGAAGAGTCAAGGACCAACATGCTGTGGCCCTGGGCAATTTCTTT	660		
661	GGTCTTTCAGTAACTGCTCTCTTCAATGGTTTAAATGATGCTTACCAACGAGTGAAG	720		
661	GGTCTTTCAGTAACTGCTCTCTTCAATGGTTTAAATGATGCTTACCAACGAGTGAAG	720		
721	TCCAAAGCTTACTCCATTTGTTGGGAAATCGACACCTGAAAAAGAGGGAGCTTGA	780		
721	TCCAAAGCTTACTCCATTTGTTGGGAAATCGACACCTGAAAAAGAGGGAGCTTGA	780		

Db	721	TCGAAAGCTACTACTGCATCTATTGTTTGTGGGAAATGCACACCTGAAAAGAGGGGAGACTTGAA	780
Qy	781	GGAATCTACTACTAAGAGCCCTGGCCCCCAAAACCAAGCTTCAAGTCCACTTCAGGCTTACAC	840
Db	781	GGAACTACTACTAAGAGCCCTGGCCCCCAAAACCAAGCTTCAAGTCCACTTCAGGCTTACAC	840
Qy	841	CCCAAGCCCTGGGGCTTCACTCCCGTGGCCAGTTCACCTTCACTCCAGCTCCCACTTATAC	900
Db	841	CCCAAGCCCTGGGGCTTCACTCCCGTGGCCAGTTCACCTTCACTCCAGCTCCCACTTATAC	900
Qy	901	CCCGGTACTGTCTCCCAACTTTTGGGGCTTCCCGCAGAGAGGTGGACACACCTATAGAGGG	960
Db	901	CCCGGTACTGTCTCCCAACTTTTGGGGCTTCCCGCAGAGAGGTGGACACACCTATAGAGGG	960
Qy	961	GCTGACCCCATCTCTTGGGACAGGCTTCGCTCCGACCCCATCCCAACCCCTTTCAGAA	1020
Db	961	GCTGACCCCATCTCTTGGGACAGGCTTCGCTCCGACCCCATCCCAACCCCTTTCAGAA	1020
Qy	1021	TGGGAGGACAGCGCCCAAGCCACAGAGCTTAGACACTGATGACCCCGCAGCTGTAC	1080
Db	1021	TGGGAGGACAGCGCCCAAGCCACAGAGCTTAGACACTGATGACCCCGCAGCTGTAC	1080
Qy	1081	GCCCTGGTGGAGAAAGGCCCCCTGGCGCTGGAAAGAAATTCGTGGGGGCGCTTAGGGCTG	1140
Db	1081	GCCCTGGTGGAGAAAGGCCCCCTGGCGCTGGAAAGAAATTCGTGGGGGCGCTTAGGGCTG	1140
Qy	1141	AGCGACACGACAGATCGATCGGCTGGAGCTGCAGAAACGGGCGCTGCCTGGCGAGGCGCAA	1200
Db	1141	AGCGACACGACAGATCGATCGGCTGGAGCTGCAGAAACGGGCGCTGCCTGGCGAGGCGCAA	1200
Qy	1201	TACAGCATGCTGGCGGACCTTGGAGGGGGCGCAGCGCGCGCGAGGCCACGCTGGAAGCTG	1260
Db	1201	TACAGCATGCTGGCGGACCTTGGAGGGGGCGCAGCGCGCGCGAGGCCACGCTGGAAGCTG	1260
Qy	1261	CTGGGACGCGGCTGCGCGCAGCATGAGCATGCTGTGGGCTGCCTGGAGAGACATCGAGGAGGCG	1320
Db	1261	CTGGGACGCGGCTGCGCGCAGCATGAGCATGCTGTGGGCTGCCTGGAGAGACATCGAGGAGGCG	1320
Qy	1321	CTTTGGCGGCCCCGCGGCGCTCCCGCGCGGCCAGTCTTCTCAGATGA	1368
Db	1321	CTTTGGCGGCCCCGCGGCGCTCCCGCGCGGCCAGTCTTCTCAGATGA	1368

RESULT 3
AAQ10883
ID AAQ10883 standard; cDNA; 2088 BP.
XX
AC AAQ10883;
XX
DT 13-MAY-1991 (first entry)
XX
DE 30KD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.
XX
KW Tumour necrosis factor; inhibitor; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
XX
PD 24-JAN-1991.
XX
PF 16-JUL-1990; 90AU-0058976.
XX
XX 07-FEB-1990; 90US-0479661.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
XX
XX (SYNE-) SYNERGEN INC.

DR	NP1: 1991-073847/11.
DR	P-PDB: AAR10986.
XX	Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT	and -beta, useful as therapeutic agent.
XX	
PS	Disclosure; Fig 21: 142pp: English.
XX	
CC	The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC	which the sequence was obt'd. was isolated from a cDNA library
CC	prep'd. from RNA form U937 cells treated with PMA/PHA. The whole
CC	gene can be inserted into expression vectors for prep. of TNF
CC	inhibitor for use in the treatment of inflammatory and degenerative
CC	diseases.
CC	See also AAQ10878, AAQ10884 and AAQ10907.
XX	
SQ	Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other:
Query Match	99.9%; Score 1366.4; DB 12; Length 2088;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 1367; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	1 ATGGGCGCTTCACCGGCTGCAGCTGCGTCCCACTGGTCTCCTGAGCTGTGGTG 60
Dd	169 ATGGGCGCTTCACCGGCTGCAGCTGCTGCTGCCGTGCTCTCTGAGCTGTGGTG 228
Oy	61 GGAAATATACCCTCAGGGGTTATTGGACTGTCCTCTCACCTAGGGGACAGGAAGAAGA 120
Dd	229 GGAAATATACCCTCAGGGGTTATTGGACTGTCCTCTCACCTAGGGGACAGGAAGAAGA 288
Oy	121 GATAGTGTGTGTCCTCCCAAGAAAATATATCCACCTCCAATAATTCATTGCTGTACC 180
Dd	289 GATAGTGTGTGTCCTCCCAAGAAAATATATCCACCTCCAATAATTCATTGCTGTACC 348
Oy	181 AAGGCGACAAGGAAGAACCTACTTGTCAATAGACTGCCAGGCCGGGGAGAGATCGGAC 240
Dd	349 AAGTGCACANAAGAACTACTTGTCAATAGACTGCCAGGCCGGGGAGAGATCGGAC 408
Oy	241 TGCAAGGAGTGTGAGACCGGCTCTTACCGCTTCAGAAAAACACCTAGACACTGCTC 300
Dd	409 TGCAAGGAGTGTGAGACCGGCTCTTACCGCTTCAGAAAAACACCTAGACACTGCTC 468
Oy	301 AGCTGCTCCAAATGCGAAGGAATGGGTCAAGTGGAGATCTCTTTGCACTGGAC 360
Dd	469 AGCTGCTCCAAATGCGAAGGAAGTGGGTCAAGTGGAGATCTCTTTGCACTGGAC 528
Oy	361 CGGGACACCGGTGTGGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAACCTT 420
Dd	529 CGGGACACCGGTGTGGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAACCTT 588
Oy	421 TTCCAGTGTCAATTGTCAGCTCTCTGCTCAATGGAGACCGTGCACCTCTCTGCCAGAG 480
Dd	589 TTCCAGTGTCAATTGTCAGCTCTCTGCTCAATGGAGACCGTGCACCTCTCTGCCAGAG 648
Oy	481 AACAGAAACACCGTGTGCACCTGCAATGCAAGGTTTTCTTTAAGAGAAAAGAGTGTGC 540
Dd	649 AACAGAAACACCGTGTGCACCTGCAATGCAAGGTTTTCTTTAAGAGAAAAGAGTGTGC 708
Oy	541 TCCTGTGTATAGTAAGAAAAGCCGTGGAGTGCAGCAATGTGTGCTATCCCACAGTTGAG 600
Dd	709 TCCTGTGTATAGTAAGAAAAGCCGTGGAGTGCAGCAATGTGTGCTATCCCACAGTTGAG 768
Oy	601 AATTTTAAGGGCACTGAGACTCAGGACACACAGTGTCTTCCCTGGTCAATTTCTTT 660
Dd	769 AATTTTAAGGGCACTGAGACTCAGGACACACAGTGTCTTCCCTGGTCAATTTCTTT 828
Oy	661 GGTCTTTGCTTTTATCCCTCTCTCATTTGTTTAAATGTATGCTTACCAAGGTGAG 720
Dd	829 GGTCTTTGCTTTTATCCCTCTCTCATTTGTTTAAATGTATGCTTACCAAGGTGAG 888
Oy	721 TCCAGCTCTACTTCATTTGTTGTGGAAATGCACACTGAAAAAGAGGGGAGCTTGAA 780
Dd	889 TCCAGCTCTACTTCATTTGTTGTGGAAATGCACACTGAAAAAGAGGGGAGCTTGAA 948

Qy	781	GGAACTACTTAAGACCCCTGGCCCCAAACCAAGCTTACAGTCCACCTCCAGGGCTTAC	844
Db	949	GGAACTACTTAAGACCCCTGGCCCCAAACCAAGCTTACAGTCCACCTCCAGGGCTTAC	1000
Qy	841	CCCAACCTGGGGCTTCAGTCCCGTGGCCGACAGTTCACCTTCACCTCCAGCTCCACCTATAC	900
Db	1009	CCCAACCTGGGGCTTCAGTCCCGTGGCCGACAGTTCACCTTCACCTCCAGCTCCACCTATAC	1060
Qy	901	CCCGGTGACTCTCCCACTTTGGGGCTTCGCCGACAGAGAGTGGACCACTTACAGGG	966
Db	1069	CCCGGTGACTCTCCCACTTTGGGGCTTCGCCGACAGAGAGTGGACCACTTACAGGG	1122
Qy	961	GCTGACCCCACTCTTTGGACAGACCCCTGGCCCTCCGACCCCACTCCCAACCCCTTCAGAG	1020
Db	1129	GCTGACCCCACTCTTTGGACAGACCCCTGGCCCTCCGACCCCACTCCCAACCCCTTCAGAG	1188
Qy	1021	TGGGAGGACAGCGCCGACACAGAGCCTAGACACTGATGACCCCGGAGCGCTGTAC	1080
Db	1189	TGGGAGGACAGCGCCGACACAGAGCCTAGACACTGATGACCCCGGAGCGCTGTAC	1248
Qy	1081	CCCGTGGTGGAGAACGTCCCCCGTTGGGCTGGGAAGAAATTCTGTGGGGCGCTTAGGGCTG	1144
Db	1249	CCCGTGGTGGAGAACGTCCCCCGTTGGGCTGGGAAGAAATTCTGTGGGGCGCTTAGGGCTG	1308
Qy	1141	AGCGACCAAGAGATCGATCGGCTGGAGGCTGAGAAAGGCGCGCTGCTGCGGGAGGCGCAA	1202
Db	1309	AGCGACCAAGAGATCGATCGGCTGGAGGCTGAGAAAGGCGCGCTGCTGCGGGAGGCGCAA	1368
Qy	1201	TACAGCATGCTGGGAGACTTGGAGGCGGGCGACGCGCGCGCGAGAGGCGACGCTGGAGCTG	1260
Db	1369	TACAGCATGCTGGGAGACTTGGAGGCGGGCGACGCGCGCGCGAGAGGCGACGCTGGAGCTG	1424
Qy	1261	CTGGGACCGCTGCTCCGGACATGAGACTGCTGGGCTGCTGGAGACATCGAGAGAGCGG	1320
Db	1429	CTGGGACCGCTGCTCCGGACATGAGACTGCTGGGCTGCTGGAGACATCGAGAGAGCGG	1488
Qy	1321	CTTTGGCGGCGCCGCGCGCCCTCCGCGCGCGCGCCAGTCTTTCAGATGA	1368
Db	1489	CTTTGGCGGCGCCGCGCGCCCTCCGCGCGCGCGCCAGTCTTTCAGATGA	1536
RESULT 4			
ID	AAC83946		
AC	AAC83946 standard; DNA; 2088 BP.		
XX	AAC83946:		
Dt	02-MAR-2001 (first entry)		
DE	Human 30 kDa TNF inhibitor precursor coding sequence.		
XX	TNF inhibitor: antiinflammatory; Tumour Necrosis Factor; Interleukin;		
KW	IL-1; Inflammatory disease; degenerative disease; human; ss.		
OS	Homo sapiens.		
XX	US6143866-A.		
PD	07-NOV-2000.		
XX	19-JAN-1995;	95US-0375242.	
XX	19-JUL-1980;	90US-0555274.	
PR	09-JUL-1983;	93US-0090366.	
PR	18-JUL-1989;	89US-0381080.	
PR	11-DEC-1989;	89US-0450329.	
PR	07-FEB-1990;	90US-0479661.	
XX	(AMGE-) AMGEN INC.		
PA	Squires C, King MW, Hale KR, Brewer MT, Thompson RC;		
PI	Vandersallice RW, Vanlice J, Kohno T;		

XX	WPI: 2001-006443/01.
DR	P-PSDB: AAB37677.
XX	
PT	Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT	non-native cysteine residue cross-linked with polyethylene glycol,
PT	useful for treating inflammatory and degenerative diseases mediated by
PT	TNF -
XX	
PS	Example 6; Fig 21; 82pp; English.
XX	
CC	The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC	(see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC	novel TNF inhibitors of the present invention are useful as therapeutic
CC	agents for inhibiting the activity of TNF and Interleukin (IL-1), and
CC	for treating inflammatory and degenerative diseases mediated by TNF. The
CC	present sequence is the coding sequence for the precursor of 30 kDa TNF
CC	inhibitor. The 30 kDa TNF inhibitor can inhibit TNF alpha.
XX	
SQ	Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;

Query Match	99.9%	Score 1366.4	DB 22	Length 2088
Best Local Similarity	99.9%	Pred. NO. 0		
Matches 1367	Conservative	0	Mismatches 1	Indels 0
			Gaps	0

QY	1	ATGGGCGCTCCACCGTGCCTCCGACCTGGTGGCTGGGAGCGTTGGTG	60
Db	169	ATGGGCGCTCCACCGTGCCTCCGACCTGGTGGCTGGGAGCGTTGGTG	228
QY	61	GGAAATATACCCCTCAGGGGGTATTGGACTGGTCCCTCACCCTAGGGGACGAGGAAGAGA	120
Db	229	GGAAATATACCCCTCAGGGGGTATTGGACTGGTCCCTCACCCTAGGGGACGAGGAAGAGA	288
QY	121	GATAGTGTGTCCCCCAAGGAAATATATCCACCCTCAAAATATATGGATTTCGTATCC	180
Db	289	GATAGTGTGTGTCCCCCAAGGAAATATATCCACCCTCAAAATATATGGATTTCGTATCC	348
QY	181	AAATGCCCAAAAGAACCTTACTTGTACATGACTGTCCAGGCCCGGGGACGATATCGAC	240
Db	349	AAATGCCCAAAAGAACCTTACTTGTACATGACTGTCCAGGCCCGGGGACGATATCGAC	408
QY	241	TGCAGGAGGTGTGAGAGGGGCTCTTCACCGCTTCAGAAAAACACCTCACAACACTGCTC	300
Db	409	TGCAGGAGGTGTGAGAGGGGCTCTTCACCGCTTCAGAAAAACACCTCACAACACTGCTC	468
QY	301	AGCTGCTCCAATATGCCGAAGAAAGAAATGGGTAGGTGAGATCTCTTCTTCACAGTGGAC	360
Db	469	AGCTGCTCCAATATGCCGAAGAAAGAAATGGGTAGGTGAGATCTCTTCTTCACAGTGGAC	528
QY	361	CGGGACACCGTGTGTGGCTGTCAGAGAAACAGTACCGGCATTTATTGAGTGAACCTT	420
Db	539	CGGGACACCGTGTGTGGCTGTCAGAGAAACAGTACCGGCATTTATTGAGTGAACCTT	588
QY	421	TTCCAGTCTTCAATTGACGCTGTGCTCAATTTGGACCGGACCTCTGCTGGCAGAG	480
Db	589	TTCCAGTCTTCAATTGACGCTGTGCTCAATTTGGACCGGACCTCTGCTGGCAGAG	648
QY	481	AAACAGAACACCGTGTGACCTGCCATGCACTGTTCTTTCTAAGAGAAAAAGAGTGTGC	540
Db	649	AAACAGAACACCGTGTGACCTGCCATGCACTGTTCTTTCTAAGAGAAAAAGAGTGTGC	708
QY	541	TTCCTGTAACTGTAAACAAAAGCCTGGAGTGCAGCAAGTTGTGCCATACCCAGATTGAG	600
Db	709	TTCCTGTAACTGTAAACAAAAGCCTGGAGTGCAGCAAGTTGTGCCATACCCAGATTGAG	768
QY	601	AATGTTAAGGGCACTGAGAGACTCAGGACCAACCACTGCTGTGGCCCTGATCATTTTCTTT	660
Db	769	AATGTTAAGGGCACTGAGAGACTCAGGACCAACCACTGCTGTGGCCCTGATCATTTTCTTT	828
QY	661	GGTCTTTGCCCTTTTATCCCTTCTCTCATTTGGTTAATGTATGTGCTACCAACGGTGGAG	720
Db	829	GGTCTTTGCCCTTTTATCCCTTCTCTCATTTGGTTAATGTATGTGCTACCAACGGTGGAG	888

Db 667 AACAGAACACCGGTGTCACCTGCCATGCAAGTTCTTTCTAAGAGAAAACGAGTGTCTC 726
 Qy 541 TCCCTGTACTACTGTAGAAAAGCCCTGAGTGCAGCAAGTGTGCTTACCCCAATGTAG 600
 Db 727 TCTGTGTACTACTGTAGAAAAGCCCTGAGTGCAGCAAGTGTGCTTACCCCAATGTAG 786
 Qy 601 AATGTAAAGGACACTGAGAGACTCAGGACACACAGTGTGTCGCCCTGATTTCTTT 660
 Db 787 AATGTAAAGGACACTGAGAGACTCAGGACACACAGTGTGTCGCCCTGATTTCTTT 846
 Qy 661 GGTCTTTGCTTTTATCCCT 720
 Db 847 GGTCTTTGCTTTTATCCCT 906
 Qy 721 TCCAAAGCT 780
 Db 907 TCCAAAGCT 966
 Qy 781 GGAACCTACTACTAGCCCTGCGCCCAAAACCAAGCTTCACTCCAGCTTCCAGC 840
 Db 967 GGAACCTACTACTAGCCCTGCGCCCAAAACCAAGCTTCACTCCAGCTTCCAGC 1026
 Qy 841 CCCACCTCTGGGCTTCACTCCGCTCCCAAGTTCACCTTCACTCCAGCTTCCAGC 900
 Db 1027 CCCACCTCTGGGCTTCACTCCGCTCCCAAGTTCACCTTCACTCCAGCTTCCAGC 1086
 Qy 901 CCCGCTGACTCTCCCAACTTTGGCGCTCCCGCAGAGAGTGTGCACCACTTACAGGG 960
 Db 1087 CCCGCTGACTCTCCCAACTTTGGCGCTCCCGCAGAGAGTGTGCACCACTTACAGGG 1146
 Qy 961 GCTGACCCCATCTTGGGACAGCCCTGCGCTCCAGCCCATCCCAACCCCTTACAGAG 1020
 Db 1147 GCTGACCCCATCTTGGGACAGCCCTGCGCTCCAGCCCATCCCAACCCCTTACAGAG 1206
 Qy 1021 TGGAGAGACAGCGCCCAACAGCCAGAGCTTACACTGATGACCCCGCAGCCTGTAC 1080
 Db 1207 TGGAGAGACAGCGCCCAACAGCCAGAGCTTACACTGATGACCCCGCAGCCTGTAC 1266
 Qy 1081 GCCCTGTGTGAGAACTGTCCCTGCTGTGAGAAAGTGTGTGCGCGCTTACAGGCTG 1140
 Db 1267 GCCCTGTGTGAGAACTGTCCCTGCTGTGAGAAAGTGTGTGCGCGCTTACAGGCTG 1326
 Qy 1141 AGCAGACAGAGATGATCGGCTGAGAGTGCAGAAACGGGCTGCTGCGAGAGCGCAA 1200
 Db 1327 AGCAGACAGAGATGATCGGCTGAGAGTGCAGAAACGGGCTGCTGCGAGAGCGCAA 1386
 Qy 1201 TACAGCATGTGCGAGACTGAGAGCGCGGCGCAGAGCCGACCTGTGAGCTG 1260
 Db 1387 TACAGCATGTGCGAGACTGAGAGCGCGGCGCAGAGCCGACCTGTGAGCTG 1446
 Qy 1261 CTGGGAGCGGCTGCTCCCGGAGATGAGACTGCTGGGCTGCTGGAGAGCATGAGAGCGG 1320
 Db 1447 CTGGGAGCGGCTGCTCCCGGAGATGAGACTGCTGGGCTGCTGGAGAGCATGAGAGCGG 1506
 Qy 1321 CTTTGGGCGCCCGCGGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
 Db 1507 CTTTGGGCGCCCGCGGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1554

RESULT 6
 AAH48859
 ID AAH48859 standard; DNA; 2111 BP.
 XX
 AC AAH48859;
 XX
 DT 12-NOV-2001 (first entry)
 XX
 DE Human TNFBP-associated DNA #1.
 XX
 TNF: tumor necrosis factor binding protein; TNFBP; treatment;
 KM insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
 KM antiprotzoal; treatment; meningococcal sepsis; cerebral malaria;
 KM autoimmune glomerulonephritis; ds.

XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Key 187..1554
 FT CDS
 FT /*tag- a
 FT /product- "TNFBP-associated protein"
 FT sig-peptide 187..270
 FT /*tag- b
 FT mat-peptide 271..1551
 FT /*tag- c
 XX
 XX EPI132471-A2.
 PD 12-SEP-2001.
 XX
 XX 31-AUG-1990; 2001EP-0108117.
 PF
 XX 12-SEP-1989; 89CH-0003319.
 PR 08-MAR-1990; 90CH-0000746.
 PR 20-APR-1990; 90CH-0001347.
 PR 31-AUG-1990; 90EP-0116707.
 PR 31-AUG-1990; 99EP-0100703.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
 PI Schlienger E;
 XX
 DR WPI: 2001-559312/63.
 DR P-PSDB; AAB86817.
 XX
 PT New homogeneous, insoluble proteins that bind tumor necrosis factor
 PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
 XX
 PS Claim 4a; Fig 1; 26pp; German.
 XX
 CC This invention describes novel insoluble proteins (i), also their
 CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
 CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
 CC invention have antiinflammatory, immunosuppressive, antibacterial,
 CC antiprotzoal activity. (i), and related recombinant proteins, are used
 CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
 CC sepsis; development of autoimmune glomerulonephritis and cerebral
 CC malaria. Also (i), or antibodies specific for them, are used for
 CC diagnostic determination of TNF in body fluids, for affinity purification
 CC of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
 CC human TNF binding protein described in the method of the invention.
 SQ Sequence 2111 BP; 447 A; 627 C; 587 G; 450 T; 0 other;

Query Match 99.98; Score 1366.4; DB 22; Length 2111;
 Best Local Similarity 99.98; Pred. No. 0;
 Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCGCTCCAGCGCTGACCTGCTGCTGCACTGATGATGCTGAGACTGTGTG 60
 Db 187 ATGGGCGCTCCAGCGCTGACCTGCTGCTGCACTGATGATGCTGAGACTGTGTG 246
 Qy 61 GGAATATACCCCTCAGGGGTTATGACTGTCTCCCTCACTAGGAGAGAGAGAGA 120
 Db 247 GGAATATACCCCTCAGGGGTTATGACTGTCTCCCTCACTAGGAGAGAGAGAGA 306
 Qy 121 GATAGTGTGTCTCCCAAGAAAATATATTCACCTCAAAATTAATTTGCTGTAC 180
 Db 307 GATAGTGTGTCTCCCAAGAAAATATATTCACCTCAAAATTAATTTGCTGTAC 366
 Qy 181 AAGTGCACAAAGAACCTACTTGTACATGATGTGTCCAGGCGCGGGGACAGATACGAC 240
 Db 367 AAGTGCACAAAGAACCTACTTGTACATGATGTGTCCAGGCGCGGGGACAGATACGAC 426
 Qy 241 TGCAGGAGTGTGAGAGCGGCTTCCACCGCTTCAAGAAAACCACTTCACTGCTC 300

Db 427 TGCAGGAGTGTGAGACGGCTCTTACACCGTTACAGAAAACACCTCAGACACTGCTC 486
 QY 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGTGAGATCTCTTCTTGCACAGTGGAC 360
 Db 487 AGCTGTCCAAATGCCGAAAGAAATGGGTGAGTGTGAGATCTCTTCTTGCACAGTGGAC 546
 QY 361 CGGAGACCGTGTGTGCTGTCAGAGAAACACAGTACCGGCTATTATTGGAGTGAACCTT 420
 Db 547 CGGAGACCGTGTGTGCTGTCAGAGAAACACAGTACCGGCTATTATTGGAGTGAACCTT 606
 QY 421 TTCCAGTGTCTAAATTTGACGCGCTCCATGGGAGCGGTGACCTCTCCGCGACGAG 480
 Db 607 TTCCAGTGTCTAAATTTGACGCGCTCTGCTCAATGGAGCCGTGACCTCTCTGCGACGAG 666
 QY 481 AAACAGAACACCGTGTGACCTGATGAGGTTCTTCTTAAGAGAAACAGTGTGTC 540
 Db 667 AAACAGAACACCGTGTGACCTGATGAGGTTCTTCTTAAGAGAAACAGTGTGTC 726
 QY 541 TCCCTAGTAACTGTAAAGAAAAGCTGAGTGCACGAAAGTTGCTTACCCAGATTGAG 600
 Db 727 TCCCTAGTAACTGTAAAGAAAAGCTGAGTGCACGAAAGTTGCTTACCCAGATTGAG 786
 QY 601 AATGTTAAGGACACTGAGACACTGACGACACAGTGTGCTGCTGCTGCTATTTCTT 660
 Db 787 AATGTTAAGGACACTGAGACACTGACGACACAGTGTGCTGCTGCTGCTATTTCTT 846
 QY 661 GGTCTTTGCTTTATTCCTCTCTTCATTTGTTAATGATATGCTTACCAAGGTGAG 720
 Db 847 GGTCTTTGCTTTATTCCTCTCTTCATTTGTTAATGATATGCTTACCAAGGTGAG 906
 QY 721 TCCAAAGCTTACTCCATTTGTTGTGGAAATGACACCTGAAAAGAGGGGAGCTTGA 780
 Db 907 TCCAAAGCTTACTCCATTTGTTGTGGAAATGACACCTGAAAAGAGGGGAGCTTGA 966
 QY 781 GGAAGTACTACTAAGGACCCCTGCGCCCAACCAAGCTTACGCTCCAGGCTTACAC 840
 Db 967 GGAAGTACTACTAAGGACCCCTGCGCCCAACCAAGCTTACGCTCCAGGCTTACAC 1026
 QY 841 CCCACCTTGGGCTTGTAGTCCCTGCGCCCAAGTTCACCTTACCTGCTCAGCTATACC 900
 Db 1027 CCCACCTTGGGCTTGTAGTCCCTGCGCCCAAGTTCACCTTACCTGCTCAGCTATACC 1086
 QY 901 CCCGCTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGTGGACACACCTATACGGG 960
 Db 1087 CCCGCTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGTGGACACACCTATACGGG 1146
 QY 961 GGTGACCCCATCTTGGCGACAGCCCTCGGCTCCGACCCCATATCCCAACCCCTTCAAG 1020
 Db 1147 GGTGACCCCATCTTGGCGACAGCCCTCGGCTCCGACCCCATATCCCAACCCCTTCAAG 1206
 QY 1021 TGGGAGAGACAGGCGCCACAGGACAGACCTAGACACTGATGACCCCGCAGAGCTGTAC 1080
 Db 1207 TGGGAGAGAGGCGCCACAGGACAGACCTAGACACTGATGACCCCGCAGAGCTGTAC 1266
 QY 1081 GCCGTGTGTGAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 Db 1267 GCCGTGTGTGAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1326
 QY 1141 AACGACACAGATGATGATGCTGTGAGTGTGAGAACGCGGCTGCTGCTGCTGCTGCTG 1200
 Db 1327 AACGACACAGATGATGATGCTGTGAGTGTGAGAACGCGGCTGCTGCTGCTGCTGCTG 1386
 QY 1201 TACAGCATCTGTGCGACCTGTGAGAGGCGGACGCGCGCGGCGGAGGCGACGCTGAGCTG 1260
 Db 1387 TACAGCATCTGTGCGACCTGTGAGAGGCGGACGCGCGCGGCGGAGGCGACGCTGAGCTG 1446
 QY 1261 CTGGAGACGCTGTCTCCGCGACATGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 Db 1447 CTGGAGACGCTGTCTCCGCGACATGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1506
 QY 1321 CTTTGGCGGCG 1368
 Db 1507 CTTTGGCGGCG 1554

RESULT 7
 ABK84039
 ID ABK84039 standard; cDNA; 2111 BP.
 XX
 AC ABK84039;
 XX
 DT 14-AUG-2002 (first entry)
 XX
 DE Human cDNA differentially expressed in granulocytic cells #610.
 XX
 KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARPS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200228999-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US30821.
 XX
 PR 03-OCT-2000; 2000US-237189P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 XX
 DR WPI: 2002-435328/46.
 XX
 PS Claim 1: SEQ ID No 610; 114bp; English.
 XX
 CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARPS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,


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PR 20-AUG-1999; 99US-149989P.
XX
XX (STRD ). UNIV LELAND STANFORD.
XX
XX
XX Rosen GD, Kao P:
XX WPI; 2002-121125/16.
XX P-PSDB; AAU75064.
XX
XX Use of a synergetic combination of death domain receptor ligands and
XX diterpenoid tripeptides for killing of tumour cells -
XX
XX Disclosure; Column 23-28; 20pp; English.
XX
XX This invention relates to a novel method for enhanced killing of tumour
XX cells comprising contacting a tumour cell with a synergetic
XX combination of a death domain receptor ligand and a diterpenoid
XX tripeptide. This method has cytostatic activity and works by blocking
XX TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the
XX invention may be used for treating tumours, particularly solid tumours,
XX e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma
XX also neurological malignancies, haematological malignancies, e.g.
XX non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant
XX cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma,
XX lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia,
XX bullous pemphigoid, discoid lupus erythematosus, lichen planus. The
XX combination may be administered with other active agents, e.g. anti-
XX metastatic, anti-tumour or anti-angiogenic agents. The potent synergy
XX between the diterpenoids and the death domain ligands allows increased
XX killing at equivalent or lower doses, and can sensitize otherwise
XX resistant cells. This sequence represents the human tumour necrosis
XX factor alpha receptor (TNF-R1) DNA. TNF-R1 is a death domain receptor
XX used in the used method of the invention in combination with diterpenoid
XX tripeptides to kill tumours by inducing apoptosis.
XX
XX Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other:
SQ
Query Match 99.9%; Score 1366.4; DB 24; Length 2161;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGCGCTCTCCACCGCTGACCTGCTGTCGCACATGTCGTCCTTGAGACCTTTGGTG 60
DB 256 ATGGGCGCTCTCCACCGCTGACCTGCTGTCGCCTGCTGCTGCTGCTGCTGCTGCTG 315
QY 61 GGAATATATACCCCTCAGGGGATTGATGATGATGATGATGATGATGATGATGATGATG 120
DB 316 GGAATATATACCCCTCAGGGGATTGATGATGATGATGATGATGATGATGATGATGATG 375
QY 121 GATAGTGTGTGTCGCCAAGGAAATATATATATATATATATATATATATATATATATAT 180
DB 376 GATAGTGTGTGTCGCCAAGGAAATATATATATATATATATATATATATATATATATAT 435
QY 181 AAGTGCACCAAGAACCTTACTTATACATGACTGTCCAGGCCGCGGGGACAGATACGGAC 240
DB 436 AAGTGCACCAAGAACCTTACTTATACATGACTGTCCAGGCCGCGGGGACAGATACGGAC 495
QY 241 TGCAGGAGTGTGAGAGCGGGTCTCTACCGGCTTACAGAAAACCACTTACAGACATGCTC 300
DB 496 TGCAGGAGTGTGAGAGCGGGTCTCTACCGGCTTACAGAAAACCACTTACAGACATGCTC 555
QY 301 AGCTGCTCCAAATGCGCAAGAAATGGTCCAGTGGAGATCTCTCTTGACACGTGGAC 360
DB 556 AGCTGCTCCAAATGCGCAAGAAATGGTCCAGTGGAGATCTCTCTTGACACGTGGAC 615
QY 361 CGGACACCGTGTGTGCTCAGAGAAAGACAGTACCGGATTAATTGGAGTGAACCTT 420
DB 616 CGGACACCGTGTGTGCTCAGAGAAAGACAGTACCGGATTAATTGGAGTGAACCTT 675
QY 421 TTCCAGTGTTCATTTGACACCTCTGCTCAATGGACCGCTGCACCTCTCTCCGACGAG 480
DB 676 TTCCAGTGTTCATTTGACACCTCTGCTCAATGGACCGCTGCACCTCTCTCCGACGAG 735

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QY 481 AAACACACACCGCTGTGACACCTGTCATGCAAGCTTCTTCTTAGAGAAAAAGAGTGTG 540
DB 736 AAACACACACCGCTGTGACACCTGTCATGCAAGCTTCTTCTTAGAGAAAAAGAGTGTG 795
QY 541 TCCTGTAGTAACTGTAAAGAAAGCCGTGAGTGCAGCAACTTGTGCTTACCACGATTTAG 600
DB 796 TCCTGTAGTAACTGTAAAGAAAGCCGTGAGTGCAGCAACTTGTGCTTACCACGATTTAG 855
QY 601 AATGTTAAGGACACGAGGACTCAGGACACACAGTGTCTTGGCCCTGCTCATTTTCTT 660
DB 856 AATGTTAAGGACACGAGGACTCAGGACACACAGTGTCTTGGCCCTGCTCATTTTCTT 915
QY 661 GGTCTTGTGCTTTTATCCCTCTCTTCAATGCTTAAATGCTTAAATGCTTAAATGCTT 720
DB 916 GGTCTTGTGCTTTTATCCCTCTCTTCAATGCTTAAATGCTTAAATGCTTAAATGCTT 975
QY 721 TCCAGCTTACTCCATTTTGTGGAAATGACACCGTGAAGAGGAGGAGGAGCTTGA 780
DB 976 TCCAGCTTACTCCATTTTGTGGAAATGACACCGTGAAGAGGAGGAGGAGCTTGA 1035
QY 781 GGAATCTACTTAAAGCCCTGCGCCCAAAACCAAGCTTCACTTCCAGCTTCAAC 840
DB 1036 GGAATCTACTTAAAGCCCTGCGCCCAAAACCAAGCTTCACTTCCAGCTTCAAC 1095
QY 841 CCCAGCTTGGGCTTCAATGTCGCTGCTCCAGTTCACCTTCACTTCACTTCACTTCAAC 900
DB 1096 CCCAGCTTGGGCTTCAATGTCGCTGCTCCAGTTCACCTTCACTTCACTTCACTTCAAC 1155
QY 901 CCCGCTGACTGTCCCACTTGTGCGCTCCGCGCAGAGAGTGGACCAACCTTATACGAG 960
DB 1156 CCCGCTGACTGTCCCACTTGTGCGCTCCGCGCAGAGAGTGGACCAACCTTATACGAG 1215
QY 961 GCTGACCCCATTCCTTGCAGACACCCCTGCTCCGACCCCATTCCTTGCAGAG 1020
DB 1216 GCTGACCCCATTCCTTGCAGACACCCCTGCTCCGACCCCATTCCTTGCAGAG 1275
QY 1021 TGGAGAGACAGCGCCCAACAGCCAGAGCTTACACTGATGACCCCGGACGCTGTAC 1080
DB 1276 TGGAGAGACAGCGCCCAACAGCCAGAGCTTACACTGATGACCCCGGACGCTGTAC 1335
QY 1081 GCGGTGTGTGAGAAAGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
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QY 1141 AGCGACACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1396 AGCGACACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1455
QY 1201 TACAGCATGCTGAGGACCTGAGAGCGGCGGACGCGCGGCGGCGGCGGCGGCGG 1260
DB 1456 TACAGCATGCTGAGGACCTGAGAGCGGCGGACGCGCGGCGGCGGCGGCGGCGG 1515
QY 1261 CTGGAGCGCTGTCTCCGAGACATGACCTGTGAGCTGCTGAGAGCATGAGAGGCG 1320
DB 1516 CTGGAGCGCTGTCTCCGAGACATGACCTGTGAGCTGCTGAGAGCATGAGAGGCG 1575
QY 1321 CTTTGGCGGCCCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
DB 1576 CTTTGGCGGCCCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1623

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RESULT 11
AAQ10955
ID AAQ10955 standard; cDNA; 2111 BP.
XX AAQ10955;
XX
XX 24-MAY-1991 (first entry)
XX Encodes human 55kD TNF-binding protein..
XX
XX Tumour Necrosis Factor; binding proteins; septic shock;
XX autoimmune glomerulonephritis; lymphokine; cytokine.
KW

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XX Key Location/Qualifiers
FH sig_peptide 187..273
FT /*tag-a
FT mat_peptide 274..1551
FT /*tag-b
FT /product= 55kd TNF-BP
XX
XX EP417563-A.
XX
XX 20-MAR-1991.
XX
XX 31-AUG-1990; 90EP-0116707.
XX
XX 20-APR-1990; 90CH-0001347.
XX 12-SEP-1989; 89CH-0003319.
XX 08-MAR-1990; 90CH-0000746.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
XX Schlaeger EJ;
XX WPI, 1991-081851/12.
XX P-PSDB; AAR11082.
XX
XX Insoluble tumour necrosis factor binding proteins - and DNA
XX encoding them, useful in pharmaceutical prods. and for antibody
XX prodn.
XX
XX Claim 4; Fig 1; 26pp; German.
XX
XX Partial amino acid sequences were determined for the 55 and 75kd
XX TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
XX synthesised based on these partial sequences. The primers were
XX used to produce a cDNA fragment for use as a probe to screen a human
XX placental cDNA bank constructed in lambda gfil1. Positive clones were
XX identified and sequenced. DNA constructs comprising the TNF-BP coding
XX sequence may also contain a fragment encoding a human Ig domain.
XX Recombinant constructs are used to transform cells to confer
XX improved TNF-binding properties.
XX See also AA010956.
XX
XX Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T; 0 other:
XX
XX Query Match 99.8%; Score 1364.8; DB 12; Length 2111;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ATGGGGCTCTCCACCGTGTGCTGACCTGTCGTCGCCACTGCTGCTCTGAGCTGTGGTG 60
XX 187 ATGGGGCTCTCCACCGTGTGCTGACCTGTCGTCGCCACTGCTGCTCTGAGCTGTGGTG 246
XX
XX 61 GGAATATTACCCCTCAGAGGGTTATTGGACTGTCCCTCACCCTAGAGGAGACAGAGAGA 120
XX 247 GGAATATTACCCCTCAGAGGGTTATTGGACTGTCCCTCACCCTAGAGGAGACAGAGAGA 306
XX
XX 121 GATAGTGTGTGTCCCAAGAGAAATATTATCCACCTCAAAATTAATTGATTGGCTGTACC 180
XX 307 GATAGTGTGTGTCCCAAGAGAAATATTATCCACCTCAAAATTAATTGATTGGCTGTACC 366
XX
XX 181 AAGTGCACAAGGAACCTACTTGTACATGTGATGCCAGGCGCGGGGAGAGATTAGGAGC 240
XX 367 AAGTGCACAAGGAACCTACTTGTACATGTGATGCCAGGCGCGGGGAGAGATTAGGAGC 426
XX
XX 241 TGCAGAGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACACCTCAGACACTGCTC 300
XX 427 TGCAGAGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACACCTCAGACACTGCTC 486
XX
XX 301 AGCTGCTCCAATATGCCGAAAGGAATGGTCAAGGTGAGATCTCTTCTTGACAGTGGAC 360
XX 487 AGCTGCTCCAATATGCCGAAAGGAATGGTCAAGGTGAGATCTCTTCTTGACAGTGGAC 546
XX
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QY 361 CGGACACCGGTGTGGTGTGACAGAGAAACAGTACCGGCATTATTGGATGAAAACTTT 420
DB 547 CGGACACCGGTGTGTGGTGTGACAGAGAAACAGTACCGGCATTATTGGATGAAAACTTT 606
QY 421 TTCCAGTGTCTCAATTGACAGCTCTGCGCTCAATGGAGCCGTGCACCTCTCTGCCAGAG 480
DB 607 TTCCAGTGTCTCAATTGACAGCTCTGCGCTCAATGGAGCCGTGCACCTCTCTGCCAGAG 666
QY 481 AAACAGAACACCGGTGTGACAGCTCTGCGCTCAATGGAGCCGTGCACCTCTCTGCCAGAG 540
DB 667 AAACAGAACACCGGTGTGACAGCTCTGCGCTCAATGGAGCCGTGCACCTCTCTGCCAGAG 726
QY 541 TCGTGTAGTACCTGTAAAGAAAAGCCGTGGAGTGCAGCAATGGCTTACCCAGATTGAG 600
DB 727 TCGTGTAGTACCTGTAAAGAAAAGCCGTGGAGTGCAGCAATGGCTTACCCAGATTGAG 786
QY 601 AATGTTAAGGGACAGTGAAGACTCAGGACACACAGTGTGCTGCTGCTGCTCAATTTCTTT 660
DB 787 AATGTTAAGGGACAGTGAAGACTCAGGACACACAGTGTGCTGCTGCTGCTCAATTTCTTT 846
QY 661 GGTCTTTGCTTTTATCCCTCTCTTCAATTTGTTTATGTATGCTTACCAAGCGTGGAG 720
DB 847 GGTCTTTGCTTTTATCCCTCTCTTCAATTTGTTTATGTATGCTTACCAAGCGTGGAG 906
QY 721 TCCAAAGCTCTACCTCCATTTGTTGGAAATGACACCTGAAAAGAGGGGGAGCTTGA 780
DB 907 TCCAAAGCTCTCTACCTCCATTTGTTGGAAATGACACCTGAAAAGAGGGGGAGCTTGA 966
QY 781 GGAACCTACTACTAAGCCCTGCGCCCAAAACCCAGCTTCCACTCCAGGCTTAC 840
DB 967 GGAACCTACTACTAAGCCCTGCGCCCAAAACCCAGCTTCCACTCCAGGCTTAC 1026
QY 841 CCCACCTTGGCTTCACTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 1027 CCCACCTTGGCTTCACTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1086
QY 901 CCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 1087 CCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1146
QY 961 GCTGACCCCATCTCTGCGACAGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 1147 GCTGACCCCATCTCTGCGACAGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1206
QY 1021 TGGAGAGACAGGCGCCACAAAGCCACAGAGCTTATGACACTGATGACCCCGGAGCTGTAC 1080
DB 1207 TGGAGAGACAGGCGCCACAAAGCCACAGAGCTTATGACACTGATGACCCCGGAGCTGTAC 1266
QY 1081 GCGGTGTGGAGAAAGTGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1267 GCGGTGTGGAGAAAGTGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1326
QY 1141 AGCGACACAGAGATCGATCGGCTGTGAGCTGACAGAAAGGCGCTGCTGCGAGCGCA 1200
DB 1327 AGCGACACAGAGATCGATCGGCTGTGAGCTGACAGAAAGGCGCTGCTGCGAGCGCA 1386
QY 1201 TACAGCATCTGCGACACTGTGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1260
DB 1387 TACAGCATCTGCGACACTGTGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1446
QY 1261 CTGGAGCGGCTGCTGCGGACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1447 CTGGAGCGGCTGCTGCGGACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1506
QY 1321 CTTTGGGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
DB 1507 CTTTGGGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1554
XX
XX RESULT 12
XX AA090513
XX ID AA090513 standard; DNA; 2175 BP.
XX
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AC AA090513;
 DT 19-JAN-1996 (first entry)
 XX
 XX
 DE p55 TNF-R gene.
 XX
 XX p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
 KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
 KM phorbol myristate acetate; PMA; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH CDS 256..1623
 FT /*tag= a
 FT /product= p55 TNF-R
 FT misc_signal 2143..2149
 FT /*tag= b
 FT /note= "possible poly-A signal"
 XX
 XX AU9475742-A.
 XX
 XX PD 04-MAY-1995.
 XX
 XX PF 11-OCT-1994; 94AU-0075742.
 XX
 XX PR 12-OCT-1993; 93IL-0107268.
 XX
 XX PA (YEDA) YEDA RES & DEV CO LTD.
 PI
 PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
 XX
 XX WPI; 1995-194342/26.
 DR
 DR P-PSDB; AAR75084.
 XX
 XX
 PT New protease capable of cleaving soluble tumour necrosis factor
 PT (TNF) receptor - from cell-bound TNF-receptor, useful for
 PT antagonising deleterious effects of TNF.
 XX
 XX
 PS Disclosure; Fig 1; 40pp; English.
 XX
 XX This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
 CC Expression of this receptor is regulated by shedding of the
 CC extracellular receptor fragment. The p55 TNF-R can be shed in response
 CC to different inducing agents, e.g. phorbol myristate acetate (PMA),
 CC depending on cell type. The only region of the receptor whose structure
 CC affects the shedding response is the spacer region (see AAR75012) in the
 CC extracellular domain. This region is located close to a site of cleavage
 CC of the molecule, and links the Cys rich module to the transmembrane
 CC domain. The spacer region of the encoded protein was used to create the
 CC chimeras between human p55 TNF-R and murine epidermal growth factor
 CC receptor (EGF-R) that are represented by AAR75007-11. This spacer region
 CC was subjected to deletion mutations (AAR75013-25) and substitutions
 CC (AAR75026-47). Of the spacer region, the most important residues are
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
 CC important of these. The shedding of the receptor is independent of the
 CC side chain identity of these residues, with the exception of a limited
 CC dependence on the identity of Val 173. Mutations which alter the
 CC conformation of the protein adversely effect the shedding process. The
 CC mutations shown in AAR75013-47 were introduced in order to create an
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
 CC AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
 CC inhibitors can be used for enhancing TNF function.
 XX
 XX
 SO Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T; 0 other;

Query Match 99.8%; Score 1364.8; DB 16; Length 2175;
 Best Local Similarity 99.9%; Pred. NO. 0;
 Matches 1366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGGCTCTCCACCGTGGCTGACCTGTGCTGCACCTGCTGCTCTCTGAGCTGTGTG 60
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D	256	ATGGGCCTCTCCACCGTCCCTGACACTCTGCTGCACGTGGTCTCTCTGGACGCTGTTGGTGC	315
Q	61	GGAAATATACCCCTCAGGGGGTTATTGACTGGTCCCTACCTAGGGGACAGGGAGAGAGA	120
D	316	GGAAATATACCCCTCAGGGGGTTATTGACTGGTCCCTACCTAGGGGACAGGGAGAGAGA	375
Q	121	GATTAGTGTGTCCCCCAAGGAAATATATCCACCCTCAAAATATTTGATTTGCTGTACC	180
D	376	GATTAGTGTGTCCCCCAAGGAAATATATCCACCCTCAAAATATTTGATTTGCTGTACC	435
Q	181	AAAGTCCCAAAAGGAACTACTTTGACAAATGACGTCCAGGGCCGGGGAGATACGGAC	240
D	436	AAAGTCCCAAAAGGAACTACTTTGACAAATGACGTCCAGGGCCGGGGAGATACGGAC	495
Q	241	TGCAAGGAGTGTGAGAGCGGCTCCCTCACCGCTTCAGAAAAACCACTTCAGACACTGCTC	300
D	496	TGCAAGGAGTGTGAGAGCGGCTCCCTCACCGCTTCAGAAAAACCACTTCAGACACTGCTC	555
Q	301	AGCTGCTCCAAATGCGCGAAAGGAATGGGTGAGTGGAGATCTCTTTGCAACAGTGCAC	360
D	556	AGCTGCTCCAAATGCGCGAAAGGAATGGGTGAGTGGAGATCTCTTTGCAACAGTGCAC	615
Q	361	CGGGACACCGGTGTGGGTGTGAGGAAACACATACCGGATTAATTTGGGTAAAAACCT	420
D	616	CGGGACACCGGTGTGGGTGTGAGGAAACACATACCGGATTAATTTGGGTAAAAACCT	675
Q	421	TTTCAGTCTTCAATTTGACAGCTTTGGCTCAATGGGACGTGCACCTCTCTGCCAGAG	480
D	676	TTTCAGTCTTCAATTTGACAGCTTTGGCTCAATGGGACGTGCACCTCTCTGCCAGAG	735
Q	481	AAACAGAACACCGGTGTGACCTGCGCATGACAGTTTCTTTCTAAGAGAAAAAGATGTGC	540
D	736	AAACAGAACACCGGTGTGACCTGCGCATGACAGTTTCTTTCTAAGAGAAAAAGATGTGC	795
Q	541	TGCTGTACTACTGTAAAGAAAAGCGTGGATGACAGAAAGTTGGCTTACCCAGATTTAG	600
D	796	TGCTGTACTACTGTAAAGAAAAGCGTGGATGACAGAAAGTTGGCTTACCCAGATTTAG	855
Q	601	AATGTTAAGGGCAGCTGAGGAGACTGAGCAGACAGTCTGTGGCCCTGTCATTTTCTTT	660
D	856	AATGTTAAGGGCAGCTGAGGAGACTGAGCAGACAGTCTGTGGCCCTGTCATTTTCTTT	915
Q	661	GGTCTTTGCCCTTTTATCCCTCTCTCTCATTTGTTTAAATGATGCTAACACGTTGAGAG	720
D	916	GGTCTTTGCCCTTTTATCCCTCTCTCTCATTTGTTTAAATGATGCTAACACGTTGAGAG	975
Q	721	TCCAAAGCTCTCTCATTTGTTTGGGAAATGACACACGAAAAAAGGGGGAGCGTTGAA	780
D	976	TCCAAAGCTCTCTCATTTGTTTGGGAAATGACACACGAAAAAAGGGGGAGCGTTGAA	1035
Q	781	GGAACTACTTAAGACCCCTGGGCCCAAAACCAAGCTTATAGTCCACTCAGAGCTTACAC	840
D	1036	GGAACTACTTAAGACCCCTGGGCCCAAAACCAAGCTTATAGTCCACTCAGAGCTTACAC	1095
Q	841	CCCAACCTGGGGCTTCAGTCCCGTGCCCGAGTTCACCTTCAACCTCCAGCTCATATACC	900
D	1096	CCCAACCTGGGGCTTCAGTCCCGTGCCCGAGTTCACCTTCAACCTCCAGCTCATATACC	1155
Q	901	CCCGGTGACTGTCCCAACTTTGGGGGCTCCCGGAGAGAGTGGACACCACTATACGGGG	960
D	1156	CCCGGTGACTGTCCCAACTTTGGGGGCTCCCGGAGAGAGTGGACACCACTATACGGGG	1215
Q	961	GCTGACCCCATCTTTGGGAGACGCGCTGCGCTCGACCCCATGCCCAACCCCTTCAGAA	1020
D	1216	GCTGACCCCATCTTTGGGAGACGCGCTGCGCTCGACCCCATGCCCAACCCCTTCAGAA	1275
Q	1021	TGGGAGGACAGCGGCCCAAGACCAAGAGCCTTAGACATGATAGACCCCGGCAAGCTGTAC	1080
D	1276	TGGGAGGACAGCGGCCCAAGACCAAGAGCCTTAGACATGATAGACCCCGGCAAGCTGTAC	1335
Q	1081	GCGCTGTGGTGAAGAACTGTCCCCCTGTGCGTGTGAAGAAATTTGCTGCGGGCTTAAAGCTG	1140
D	1336	GCGCTGTGGTGAAGAACTGTCCCCCTGTGCGTGTGAAGAAATTTGCTGCGGGCTTAAAGCTG	1395

QY 961 GCTGACCCCATCTTGGCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
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 Db 1115 GCTGACCCCATCTTGGCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1174
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 QY 1021 TGGGAGGACAGCGCCCAACAGCCAGAGCTAGACATGATGACCCCGCAGCTGTAC 1080
 |||||
 Db 1175 TGGGAGGACAGCGCCCAACAGCCAGAGCTAGACATGATGACCCCGCAGCTGTAC 1234
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 Db 1235 GCCGTGTGTGAGAAAGCTGCCCGCTTGGCGTGAAGAATTCGTGCGCGCTAGAGCTG 1294
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 QY 1141 AGCAGCAGAGATGATGAGCTGGAGCTGCAGAAAGGCGCTGCTCGCGAGCGCAA 1200
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 Db 1295 AGCAGCAGAGATGATGAGCTGGAGCTGCAGAAAGGCGCTGCTCGCGAGCGCAA 1354
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 QY 1201 TACAGCATGCTGGGAGCTGAGAGCGGCGCACGCCGCGCGAGAGCCAGCTGAGCTG 1260
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 Db 1355 TACAGCATGCTGGGAGCTGAGAGCGGCGCACGCCGCGCGAGAGCCAGCTGAGCTG 1414
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 QY 1261 CTGGGAGCGCTGCTCCGCGAGATGAGCTGCTGGGCTGCTGGAGGACATGAGAGGCG 1320
 |||||
 Db 1415 CTGGGAGCGCTGCTCCGCGAGATGAGCTGCTGGGCTGCTGGAGGACATGAGAGGCG 1474
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 QY 1321 CTGTCG 1368
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 Db 1475 CTGTCG 1522
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RESULT 14
 AAQ24440
 ID AAQ24440 standard; DNA: 2062 BP.

XX
 AC AAQ24440;

DT 05-NOV-1992 (first entry)

XX
 DE Encodes TNF-alpha 55kD receptor.

XX
 KM tumour necrosis factor alpha: extracellular binding domain;

KM
 KM treatment: pulmonary diseases; septic shock; HIV infection; AIDS;

KM
 KM malaria; viral meningitis; graft versus host disease;

XX
 KM autoimmune disease; rheumatoid arthritis.

OS
 XX Homo sapiens.

XX
 FH Key

FT CDS

FT 156..1517

FT /tag- a

FT /product- human TNF-alpha

FT 1265..1267

FT /tag- b

FT /note- "3"

FT 1265..1267

FT /tag- c

FT /codon- seq: "TGG", aa: Thr

FT 1258..1260

FT /tag- d

FT /codon- Seq "AAG", aa: Leu

FT 1433..1435

FT /tag- e

FT /codon- Seq: "GAC", aa: Asn

FT 156..274

FT /tag- f

XX sig_peptide

XX W09207076-A.

XX 30-APR-1992.

XX 18-OCT-1991.

XX 91MO-GB01826.

XX 18-OCT-1990.

PR 90GB-0022648.

XX
 PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
 XX
 PI Brennan FM, Feldmann M, Gray PM, Turner MJC:
 XX
 DR WPI: 1992-167156/20.
 DR P-PSDB: AAR24000.
 XX
 PT New polypeptide capable of binding human TNF alpha - comprises
 PT first three cysteine-rich subdomains of TNF alpha receptor for
 PT treating autoimmune disease, septic shock, HIV etc.
 XX
 PS Claim 4; Fig 1; 43pp: English.
 XX
 CC This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA
 CC library in gl10 was screened with probe AAQ29236. Ten hybridising clones
 CC were plaque purified and cDNA size determined by PAGE against an
 CC Eco RI digested phage DNA. The inserts of two cDNA clones were then
 CC sequenced. The coding region of the majority of the human TNF-alpha
 CC 55kD receptor was isolated as an EcoRI fragment encoding 374 amino
 CC acids, and cloned into a mammalian cell expression vector, resulting
 CC in pTNFR. A derivative of the TNF-alpha receptor was produced by
 CC engineering a termination codon just prior to the transmembrane
 CC domain. PCR with primers AAQ29237,8 generated a 300bp
 CC restriction fragment which was cloned into pTNFR, giving pTNFRcd.
 CC DNA sequencing confirmed this contained the designed DNA sequence.
 CC The TNF-alpha receptor expression plasmids were then transfected
 CC into monkey COS-7 cells.
 CC See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8
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 SQ Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T; 0 other;

Query Match 99.6%; Score 1363.2; DB 13; Length 2062;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 215 GGAATATACCCCTCAGGGGTATTGAGCTGTCCCTCACTTGAAGGACAGGAGAAAGA 274
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 Db 575 TTCCAGTCTTCAATTGACAGCTTGCCTCAATGGACCGTGCACCTCTCTGCAAGAG 634
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Oy 661 GGTCTTTGCTCTTTATCCCTCTTCATTTGTTTAAATATATGCTACCAAGGTGAAG 720
Db 815 GGTCTTTGCTCTTTATCCCTCTTCATTTGTTTAAATATATGCTACCAAGGTGAAG 874
Oy 721 TCCAAGCTCTACTCCATTTGTTTGGGAAATGACACCTGAAAAGAGGGAGCTTGA 780
Db 875 TCCAAGCTCTACTCCATTTGTTTGGGAAATGACACCTGAAAAGAGGGAGCTTGA 934
Oy 781 GGAATCTACTACTAACCCCTGGCCCCCAAAACCAAGCTTACGCTCCACTCAGCTTAC 840
Db 935 GGAATCTACTACTAACCCCTGGCCCCCAAAACCAAGCTTACGCTCCACTCAGCTTAC 994
Oy 841 CCCACCTGGGCTTACGATCCGTCGACAGTTCACCTTACCTCCAGCTCCACCTATACC 900
Db 995 CCCACCTGGGCTTACGATCCGTCGACAGTTCACCTTACCTCCAGCTCCACCTATACC 1054
Oy 901 CCCGCTGACTGTCCCAACTTTTGGGCTCCCGCAGAGAGGTGGACACACCTATCAGGG 960
Db 1055 CCCGCTGACTGTCCCAACTTTTGGGCTCCCGCAGAGAGGTGGACACACCTATCAGGG 1114
Oy 961 GCTGACCCCATCTCTTGGCAGACCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAA 1020
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Db 1175 TGGGAGACAGCGCCACACAGCCACAGACCTAGACACTGATGACCCCGCAGCGCTGAC 1234
Oy 1081 GCCGTGTGAGAGACGTGCCCCCGCTTGGCGCTGGAAGGAATTCGTGCGGCGCTAGGGCTG 1140
Db 1235 GCCGTGTGAGAGACGTGCCCCCGCTTGGCGCTGGAAGGAATTCGTGCGGCGCTAGGGCTG 1294
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Db 1355 TACAGCATGCTGGCGACCTGGAGGGGCGCAGCGCGCGGAGGCGCAGCTGGAGCTG 1414
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Db 1415 CTGGGACGGCTGCTCGCGACATGAGACCTGTGGGCTGCTGAGAGACATCGAGAGGCG 1474
Oy 1321 CTTTGGGGGGCGCGCGCTCCCGCGCGCGCGCCAGTCTTCTCAGATGA 1368
Db 1475 CTTTGGGGGGCGCGCGCTCCCGCGCGCGCGCCAGTCTTCTCAGATGA 1522

```

RESULT 15

AAQ12215 standard: DNA: 2176 BP.

AAQ12215;

12-SEP-1991 (first entry)

Type I TNF receptor.

Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.

Homo sapiens.

Key Location/Qualifiers

FT terminator 244..246 /*tag= a

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FT CDS /note= "in-frame termination codon"
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FT FT /*tag= a
FT FT /product= type I TNF receptor
FT FT 256..318
FT FT /*tag= b
FT FT 319..1620
FT FT mat_peptide
FT FT /*tag= c
FT FT 319..864
FT FT misc_RNA
FT FT /*tag= d
FT FT /label= soluble_domain
FT FT /note= "may be 2 codons shorter or a few codons longer"
FT FT misc_feature
FT FT 376..414
FT FT /*tag= e
FT FT /note= "TBP-I derived sequence"
FT FT 583..627
FT FT /*tag= f
FT FT /note= "TBP-I derived sequence"
FT FT 850..858
FT FT misc_feature
FT FT 859..957
FT FT /*tag= g
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FT FT /label= transmembrane_domain
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FT FT /*tag= i
FT FT /number= 1
FT FT 505..633
FT FT /*tag= j
FT FT /number= 2
FT FT 634..756
FT FT repeat_unit
FT FT /*tag= k
FT FT /number= 3
FT FT 757..858
FT FT repeat_unit
FT FT /*tag= l
FT FT /number= 4
FT FT 2145..2150
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FT FT /*tag= m
FT FT EP433900-A.
FT FT 26-JUN-1991.
FT FT PD 13-DEC-1990; 90BP-0124133.
FT FT PF 12-JUL-1990; 90IL-0095064.
FT FT PR 13-DEC-1989; 89IL-0092697.
FT FT XX
FT FT (YEDA ) YEDA RES & DEV CO LTD.
FT FT PA
FT FT PI Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
FT FT PI Aderka D;
FT FT PI WPI: 1991-186774/26.
FT FT DR P-PSDB; AAR12550.
FT FT XX
FT FT XX Recombinant tumour necrosis factor binding protein I - prepd. by
FT FT PT transfecting eukaryotic cells with vector contg. deoxyribonucleic
FT FT PT acid encoding human type I TNF receptor or soluble domain
FT FT XX
FT FT PS Disclosure: Fig 1(D): 30pp: English.
FT FT XX
FT FT XX The Tumour Necrosis Factor Binding Protein I is the soluble form of
FT FT CC type I TNF-receptor and constitutes a fragment of the cell surface
FT FT CC form of this receptor, corresp. to its extracellular domain.
FT FT CC There is no characteristic poly(A) addition signal near the 3' end
FT FT CC of the cDNA. The sequence ACTAAA (tag m) may serve as an
FT FT CC alternative to this signal, but with low efficiency.
FT FT CC See also AAQ12212-15.
FT FT XX
FT FT XX Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T; 0 other;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2002, 19:16:35 : Search time 2817 Seconds

(without alignments)
14132.992 Million cell updates/sec

Title: US-09-899-429a-1

Perfect score: 1368

Sequence: 1 atggcgctctccacgcgtgc.....cgccacgctcttcacgatga 1368

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : GenEmbl:

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_ov:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_ph:*

24: em_pat:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rtd:*

36: em_htg_mem:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	1368	100.0	1368	6	A29098	A29098 Synthetic D
2	1368	100.0	2112	9	HUMTNFRC	M63121 Human tumor
3	1368	100.0	2194	9	BC010140	BC010140 Homo sapi
4	1366.4	99.9	2087	9	HUMTNFR	A33294 Human tumor
5	1366.4	99.9	2111	6	A26412	A26412 cDNA for (5
6	1366.4	99.9	2111	6	AX409713	AX409713 Sequence
7	1366.4	99.9	2111	6	HUMTNFRP	M58286 Homo sapien
8	1366.4	99.9	2161	6	AR063330	AR063330 Sequence
9	1366.4	99.9	2161	9	HSTNFR1A	X55313 H. sapiens T
10	1366.4	99.9	2175	6	A43873	A43873 Sequence 1
11	1366.4	99.9	2175	6	A78738	A78738 Sequence 7
12	1366.4	99.9	2175	6	AR041076	AR041076 Sequence
13	1366.4	99.9	2175	6	164751	164751 Sequence 1
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17	1351.2	98.8	2061	6	A20255	A20255 55kd recept
18	1344.4	98.3	2109	9	AK056611	AK056611 Homo sapi
19	1323.2	96.7	2050	9	HUMTNFRP	M60275 Human tumor
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21	890.6	65.1	2171	4	AB051103	AB051103 Fells cat
22	861	62.9	2004	4	SSU19994	U19994 Sus scrofa
23	743.4	54.3	2115	10	AF329976	AF329976 Rattus no
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34	690.4	50.5	2068	10	BC004599	BC004599 Mus muscu
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36	690.4	50.5	2179	10	MMTNFR5	X57796 Mouse mRNA
37	685.4	50.1	2440	4	BTU0937	U90937 Bos taurus
38	632.8	46.3	6896	6	AR031375	AR031375 Sequence
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40	632.4	46.2	6889	6	I26928	I26928 Sequence 2
41	596.8	43.6	600	6	A20257	A20257 Synthetic n
42	593.6	43.4	600	6	I43808	I43808 Sequence 47
43	514	37.6	1301	6	AR131310	AR131310 Sequence
44	514	37.6	1301	6	AR134762	AR134762 Sequence
45	510	37.3	510	6	A21525	A21525 Oligonucleo

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
A29098	A29098	Synthetic DNA for TNF-receptor from patent EP0393438.	A29098	A29098.1	GI:1248892	.	synthetic construct.	1 (bases 1 to 1368)	Hauptmann,R., Himmeler,A., Maurer-Fogy,I. and Stratowa,C.	TNF-receptor, TNF-binding protein and DNA coding therefor	Patent: EP 0393438-A 48 24-OCT-1990;
							artificial sequences.		BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H		

Pred. No. is the number of results predicted by chance to have a

BASE COUNT	ORIGIN	FEATURES	COMMENT	MEDLINE
433 a	624 c	581 g	449 t	900335285 2158863 PUBMED
<p>Drift entry and computer-readable sequence for [1] kindly submitted by T. Schall, 26-MAR-1990.</p> <p>Location/Qualifiers</p> <p>1..2087</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>182..1549</p> <p>/note="tumor necrosis factor receptor"</p> <p>/codon_start=1</p> <p>/protein_id="AA03210.1"</p> <p>/db_xref="GI:339745"</p> <p>/translation="MGLSTVDDLLPLVLELIVGIVPSGVIGLVPHLGDREKRDVSC PGGYTHPNNISICTCKCHKGTLYLNDPCPGQDTPDREBSGFTASNNHLRCLSC SKCKREMGQVEIISCTVDRDTPVCGCRNORYRHWSENLFCFNCSLCINLTVHLSCE KONTVCCTCHAGFLIRENECVSCNSCKSLCTCKLCLPOLIENVKCTEDSGTVELPLVI FFGCLLSLFTIGLMRYORWMSKLYIVCGKSPREKEGELEGATTKPLAPNPSFT PGPFLTGFSPSPSTSTSYVPGCCPNPAAFRREVADPYOGADPILADALASPT PNIPLQKWDSSAKHPOSILDTDDPALVIVVENVPILPKKFEVYRLGSLSDHIDIRELON GRCLEADQVSHLAVRRRRTRRRENTTELLGVLADMDLGLCEDIEEALCGPALPPA PSLLR"</p>				

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Best Local	Similarity	99.9%	Pred. No. 2.1e-255:		
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QY	61	GGAATATCCCTCCAGGGGTTATTGGACTGTGCTCCACTAAGGGGAAGGAAGA	120		
Db	242	GGAATATCCCTCCAGGGGTTATTGGACTGTGCTCCACTAAGGGGAAGGAAGA	301		
QY	121	GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATTAATTCATTGTGCTGACC	180		
Db	302	GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATTAATTCATTGTGCTGACC	361		
QY	181	AAGTCCCAAAAAGAACTACTTGTATCAATATACTTCCAGGCCCGGGGACAGATACGAC	240		
Db	362	AAGTCCCAAAAAGAACTACTTGTATCAATATACTTCCAGGCCCGGGGACAGATACGAC	421		
QY	241	TGCAGGAGTGTGAGAGCGGCTCTTTCACCGCTTGAGAAAAACACCTAGACACTGCTC	300		
Db	422	TGCAGGAGTGTGAGAGCGGCTCTTTCACCGCTTGAGAAAAACACCTAGACACTGCTC	481		
QY	301	AGCTCTCCAAATGCGGAAAGAAATGGGTGACGTGAGATCTCTTTCGACAGTGGAC	360		
Db	482	AGCTCTCCAAATGCGGAAAGAAATGGGTGACGTGAGATCTCTTTCGACAGTGGAC	541		
QY	361	CGGGACACCGTGTGGGTGCGAGAAACAAGTACGGGCAATTATGGAGTGAACCTT	420		
Db	542	CGGGACACCGTGTGGGTGCGAGAGAAACCAATACGGGCAATTATGGAGTGAACCTT	601		
QY	421	TTCAGTCTTCATATGGACCTCTGCTCTCAATGGGACCGTGCACCTCTCTCCAGGAG	480		
Db	602	TTCAGTCTTCATATGGACCTCTGCTCTCAATGGGACCGTGCACCTCTCTCCAGGAG	661		
QY	481	AAACGAACACCGTGTGCACCTGCGCATGACAGTTTCTTTTAAAGAAAAAGAGTGTGC	540		
Db	662	AAACGAACACCGTGTGCACCTGCGCATGACAGTTTCTTTTAAAGAAAAAGAGTGTGC	721		
QY	541	TCTCTAGTAACTGTAAAGAAAGCCTGGAAGTGCAGGAAGTGTGCACTACCCAGATTGAG	600		
Db	722	TCTCTAGTAACTGTAAAGAAAGCCTGGAAGTGCAGGAAGTGTGCACTACCCAGATTGAG	781		
QY	601	AATGTTAAGGACACTGAGGACACTAGGACACACAGTGTCTTGGCCCTGTCATTTTCTTT	660		
Db	782	AATGTTAAGGACACTGAGGACACTAGGACACACAGTGTCTTGGCCCTGTCATTTTCTTT	841		

QY	661	GGTCTTTGGCCTTTTATTCCTCTCTCTTCAATTGGTTTAATGTATCGGTACCAACGGGTGAA	720
Db	842	GGTCTTTGGCCTTTTATTCCTCTCTCTTCAATTGGTTTAATGTATCGGTACCAACGGGTGAA	901
QY	721	TCCAAAGCTCTACTGCATTGTTTGGGAAATCGACACCTGTAAAAAGAGGGGAGCTTGA	780
Db	902	TCCAAAGCTCTACTGCATTGTTTGGGAAATCGACACCTGTAAAAAGAGGGGAGCTTGA	961
QY	781	GGAACTACTACTAAGCCCGCTGGCCCAAAACCCAAAGCTTCACTCCCACTCCAGGCTTACC	840
Db	962	GGAACTACTACTAAGCCCGCTGGCCCAAAACCCAAAGCTTCACTCCCACTCCAGGCTTACC	1021
QY	841	CCCACTCTGGGCTTAGTCCGCTGCCAGTTTCACCTTCACCTCCAGCTTCCACCTATAC	900
Db	1022	CCCACTCTGGGCTTAGTCCGCTGCCAGTTTCACCTTCACCTTCACCTCCAGCTTATACC	1081
QY	901	CCCGGTGACTGTGCCCACTTTGGCGGCTCCCGGAGAGAGTGGGACCAACCCATTCAGGG	960
Db	1082	CCCGGTGACTGTGCCCACTTTGGCGGCTCCCGGAGAGAGTGGGACCAACCCATTCAGGG	1141
QY	961	GCTGACCCCATTCCTTGGCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG	1020
Db	1142	GCTGACCCCATTCCTTGGCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG	1201
QY	1021	TGGGAGGACAGCGCCCAACAGCCACAGACCTAGACACTGATGACCCCGCAGCCTGTAC	1080
Db	1202	TGGGAGGACAGCGCCCAACAGCCACAGACCTAGACACTGATGACCCCGCAGCCTGTAC	1261
QY	1081	GCCGTGTGGAGAACGTGCCCCCTTGGGCTGGGAGAAATTCGTCCGGCGCTTAGGGCTG	1140
Db	1262	GCCGTGTGGAGAACGTGCCCCCTTGGGCTGGGAGAAATTCGTCCGGCGCTTAGGGCTG	1321
QY	1141	AGCGACCAAGAGATGATGCTGCGCTGAGCTGAGAGACGGGCGCTCGCGAGAGCGCAA	1200
Db	1322	AGCGACCAAGAGATGATGCTGCGCTGAGCTGAGAGACGGGCGCTCGCGAGAGCGCAA	1381
QY	1201	TACAGCATGCTGGGAGCACTGTGAGCGCGGCGACCGCGCGGAGAGCAAGCTGAGCTG	1260
Db	1382	TACAGCATGCTGGGAGCACTGTGAGCGCGGCGACCGCGCGGAGAGCAAGCTGAGCTG	1441
QY	1261	CTGGGACGGGTCTCTCGGGACATGGACCTGCGGGCTCGCTGGAGAGACATGGAGAGGCG	1320
Db	1442	CTGGGACGGGTCTCTCGGGACATGGACCTGCGGGCTCGCTGGAGAGACATGGAGAGGCG	1501
QY	1321	CTTTGCGGCGCCCGCGCCCTCCCGCGCGCGCCAGCTCTTCAGATGA	1368
Db	1502	CTTTGCGGCGCCCGCGCCCTCCCGCGCGCGCCAGCTCTTCAGATGA	1549
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DEFINITION	CDNA for (55KD TNF-BP) tumor necrosis factor binding protein from		
ACCESSION	A26412		
VERSION	A26412.1	GI:904968	
KEYWORDS			
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
CDS			

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Query Match	99.98;	Score 1366.4;	DB 6;	Length 2111;
Best Local Similarity	99.98;	Pred. No. 2.1e-265;		
Matches 1367; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

OY	1	ATGGGCGCTCTCCACCGTGGCCGACCTGCTCTGTGGCACTGGTGGTCCCGTGGAGCGTTGGTG	60
Db	187	ATGGGCGCTCTCCACCGTGGCCGACCTGACCTCTGTGTGCCGTGGTGTCTCTGGAGCGTGGTG	246
OY	61	GGAAATATACCCCTCAGGGGGTATTGGAGCTGAGTCCCTCACCCTAGGGGACAGAGGAAGAG	120
Db	247	GGAAATATACCCCTCAGGGGGTATTGGAGCTGGTCCCTCACCCTAGGGGACAGAGGAAGAG	306
OY	121	GATAGTGTGTGTCCCCCAAGGAAATATATCCACCCTCAAAATATATTCGATTGTCTTACC	180
Db	307	GATAGTGTGTGTCCCCCAAGGAAATATATCCACCCTCAAAATATATTCGATTGTCTTACC	366
OY	181	AAGTGCACCAAGGAAACCTACTTGTACAAATGACGTGCAGGCGCGGGGGAGGATATAGGAC	240
Db	367	AAGTGCACCAAGGAAACCTACTTGTACAAATGACGTGCAGGCGCGGGGGAGGATATAGGAC	426
OY	241	TGCAGGGAGTGTGAGAGCGGCTCTTACACCGCTTCAGAAAACCAACCTCAGACACTGCTC	300
Db	427	TGCAGGGAGTGTGAGAGCGGCTCTTACACCGCTTCAGAAAACCAACCTCAGACACTGCTC	486
OY	301	AGCTGCTCAAAATGCCGAAAGGAATGGGTGAGGTGAGATCTCTTCTTGACAGTGGAC	360
Db	487	AGCTGCTCAAAATGCCGAAAGGAATGGGTGAGGTGAGATCTCTTCTTGACAGTGGAC	546
OY	361	CGGGACACCGGTGTGTGGCTGTGAGAGAAACACGATACCGGATATTGAGATGAAAACTT	420
Db	547	CGGGACACCGGTGTGTGGCTGTGAGAGAAACACGATACCGGATATTGAGATGAAAACTT	606
OY	421	TTCCAGTCCCTCAATTGAGCGCTGTGGCTCAATGGGACGGTGGACCGTCTGTCCAGAGAG	480
Db	607	TTCCAGTCCCTCAATTGAGCGCTGTGGCTCAATGGGACCGTGGACCGTCTGTCCAGAGAG	666
OY	481	AAACGAAACACCGTGTGACACTGCGCATGACGAGTTCTTTTAGAGAAAAAGAGTGTGTC	540
Db	667	AAACGAAACACCGTGTGACACTGCGCATGACGAGTTCTTTTAGAGAAAAAGAGTGTGTC	726
OY	541	TCCTGTAGTAACTGTAAAGAAAAAGCCTGAGTGCACGAGATTGTGTCTACCCAGATTGAG	600
Db	727	TCCTGTAGTAACTGTAAAGAAAAAGCCTGAGTGCACGAGATTGTGTCTACCCAGATTGAG	786
OY	601	AATGTTAAGGGCACTGAGGAGCTCAGGACCAACAGTGTGTGGCCCGCTGGCATTTTCTTT	660
Db	787	AATGTTAAGGGCACTGAGGAGCTCAGGACCAACAGTGTGTGGCCCGCTGGCATTTTCTTT	846
OY	661	GATCTTTACCTTTTATCCCTCTCTTCAATTGGTTAATGATGCTACCAACGGTGGAG	720
Db	847	GATCTTTACCTTTTATCCCTCTCTTCAATTGGTTAATGATGCTACCAACGGTGGAG	906
OY	721	TCCAAAGCTACTCATCTGTTGTTGGGAAATCGACACCTCAAAAAAGAGGGGGAGCTTGAA	780
Db	907	TCCAAAGCTACTCATCTGTTGTTGGGAAATCGACACCTCAAAAAAGAGGGGGAGCTTGAA	966
OY	781	GGAACTACTACTAAGCCCGTGGCCCAAAACCAAGCTTCAGTCCCACTCAGGCTTCACC	840

Db	967	GGAACTACTAATGAAGCCCTGGGCCCCAAAGCCAAAGCTTGAATGCCACTTCAGGCTTCACC	1026
QY	841	CCCAACCCCTGGGCTTCACTGCCGTGGCCAGTTCACCTTACTCCAGCTCCACCTATAC	900
Db	1027	CCCAACCCCTGGGCTTCACTGCCGTGGCCAGTTCACCTTCACTCCAGCTCCACCTATAC	1086
QY	901	CCCGGTACACTGTCCCACTTTGGGGCTCCCCGAGAGAGTGTGGCAACCCATATAGGGG	960
Db	1087	CCCGGTACACTGTCCCACTTTGGGGCTCCCCGAGAGAGTGTGGCAACCCATATAGGGG	1146
QY	961	GCTAACCCTCATCTTTGGGAGACGCCCTTGCCCTCGACCCCATCCCAACCCCTTTCAGAG	1020
Db	1147	GCTAACCCTCATCTTTGGGAGAGGCCCTTGCCCTCGACCCCATCCCAACCCCTTTCAGAG	1206
QY	1021	TGGGAGGACAGCGCCCAAGGACCAAGAGGCTTAGACATGATAGACCCGCGAGCTGTAC	1080
Db	1207	TGGGAGGACAGCGCCCAAGGACCAAGAGGCTTAGACATGATAGACCCGCGAGCTGTAC	1266
QY	1081	GCCGTGGTGGAGAACTGTCCCCCGTTGGCTGTGAGAGGAATTTGTCGGGCGCTAGGGCTG	1140
Db	1267	GCCGTGGTGGAGAACTGTCCCCCGTTGGCTGTGAGAGGAATTTGTCGGGCGCTAGGGCTG	1326
QY	1141	AGGCACCAAGAGATCATGTGGGCTGGAGAGCTGCAAAAGGGCGCTGGCTGGCGAGGCGCA	1200
Db	1327	AGGCACCAAGAGATCATGTGGGCTGGAGAGCTGCAAAAGGGCGCTGGCTGGCGAGGCGCA	1386
QY	1201	TACAGACATGTGAGGACTCTGGAGGGCGGCGACGCCCGCGCGAGAGCCACGCTGGAGCTG	1260
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QY	1261	CTGGGACGCGTGTCTCGCGGACATGAGACTTGTGGCTGCTCTGAGAGACATGAGAGGCGG	1320
Db	1447	CTGGGACGCGTGTCTCGCGGACATGAGACTTGTGGCTGCTGAGAGACATGAGAGGCGG	1506
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DEFINITION	Sequence 2360 from Patent WO0229103.		
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KEYWORDS
SOURCE
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ORGANISM Homo sapiens; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1
AUTHORS Alvaras,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 2360 11-APR-2002;

GENE.LOGIC INC (US)	location/Qualifiers
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source	

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Best Local Similarity	99.9%;	Pred. No. 2.1e-265;		
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QY 61 GGAATATACCCCTCAGGGGTTATTGGACTGTCCTCTACCTAGGGGACAAGGAGAGAGA 120

Dh 247 GGAATATACCCCTGAGGGGTTATTGAGTGGTCCCTCACCTAGGGAGCAGGGAGAGAGA 306
Oy 121 GATAGTGTGTGCCCAAGGAAATATATTCACCTCTCAAAATTAATTCATTTTGTGTACC 180
Dh 307 GATAGTGTGTGCCCAAGGAAATATATTCACCTCTCAAAATTAATTCATTTTGTGTACC 366
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DEFINITION M58286 M33480
ACCESSION M58286.1 GI:339753
VERSION
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SOURCE Human cell line HL60, CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2111)
AUTHORS Loetscher, H., Pan, Y.C., Lahm, H.W., Gentz, R., Brockhaus, M., Tabuchi, H., and Lesslauer, W.
TITLE Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor
JOURNAL Cell 61 (2), 351-359 (1990)
MEDLINE 90235284
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Oy 121 GATATGTGTGTCGCCAAGGAAATATATCCACCCCAAAATATATGATTTGCTGTACC 180
Db 307 GATATGTGTGTCGCCAAGGAAATATATCCACCCCAAAATATATGATTTGCTGTACC 366
Oy 181 AAGTGCACAAAGAACCTTCTGTACAAATGACTGTGCAGGCCCGGGGAGAGATACGAGC 240
Db 367 AAGTGCACAAAGAACCTTCTGTACAAATGACTGTGCAGGCCCGGGGAGAGATACGAGC 426
Oy 241 TGCAGGAGAGTGTAGAGAGCGGCTCCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 300
Db 427 TGCAGGAGAGTGTAGAGAGCGGCTCCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 486
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Db 487 AGCTGCTCCAAATGCCCAGAAAGAAATGAGTGTGAGATCTCTTTTGCACAGTGGAC 546
Oy 361 CGGAGACACCGTGTGTGCTGCAGGAAAGAACCACTACCGCATTTAGAGTGAACCTT 420
Db 547 CGGAGACACCGTGTGTGCTGCAGGAAAGAACCACTACCGCATTTAGAGTGAACCTT 606
Oy 421 TTCCAGTGTCTCAATTCGACCTCTGCTTAATGGACCGTGCACCTCTCTCCAGAGAG 480
Db 607 TTCCAGTGTCTCAATTCGACCTCTGCTTAATGGACCGTGCACCTCTCTCCAGAGAG 666
Oy 481 AAACAGAACACCGGTGTGCTGCACCTGCATGCAAGTGTCTTTTAAAGAGAAACGAGTGTGTC 540
Db 667 AAACAGAACACCGGTGTGCTGCACCTGCATGCAAGTGTCTTTTAAAGAGAAACGAGTGTGTC 726
Oy 541 TCTGTAGTAACTGTAAAGAAACCTGAGTGCACGAAATGTGTGCTTACCCAGATTGAG 600
Db 727 TCTGTAGTAACTGTAAAGAAACCTGAGTGCACGAAATGTGTGCTTACCCAGATTGAG 786
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Db 787 AATGTTAAGGGGCACTGAGGACTCAGGCACCACTGCTGTGGCCCTGGTCAATTTCTTT 846
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Db 907 TCCAAGCTACTCATTTGTTGTGGGAAATGCACACCTGAAAAAGAGGGGAGCTTGAA 966
Oy 781 GGAATCTACTTAAGCCCTCGGGCCCAAAACCAAGCTTCACTGCTCCAGCTTCAC 840
Db 967 GGAATCTACTTAAGCCCTCGGGCCCAAAACCAAGCTTCACTGCTCCAGCTTCAC 1026
Oy 841 CCCACCTGCGGCTTCAGTCCGTCGCCAGTTCACCTTCACCTCCAGCTTCATATAC 900
Db 1027 CCCACCTGCGGCTTCAGTCCGTCGCCAGTTCACCTTCACCTCCAGCTTCATATAC 1086
Oy 901 CCCGCTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGGTGGCACCACTTCACAGGG 960
Db 1087 CCCGCTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGGTGGCACCACTTCACAGGG 1146
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Db 1447 CTGGAGACGCTGTCCGCGACATGAGACTGTGAGGCTGTCTGAGAGACATCGAGAGGCG 1506
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RESULT 8
LOCUS AR096330 2161 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 6007995.
ACCESSION AR096330
VERSION AR096330.1 GI:10025045
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2161)
AUTHORS Baker,B.F. and Cowser,L.M.
TITLE Antisense inhibition of TNF α expression
JOURNAL Patent: US 6007995-A 1 28-DEC-1999;
FEATURES
source location/Qualifiers
1..2161 /organism="unknown"
BASE COUNT 459 a 642 c 604 g 456 t
ORIGIN

Query Match 99.9%; Score 1366.4; DB 6; Length 2161;
Best Local Similarity 99.9%; Pred. No. 2.1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 9
LOCUS HSTNFR1A 2161 bp mRNA linear PRI 18-JAN-1993
DEFINITION H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.
ACCESSION X53313
VERSION X53313.1 GI:37223
KEYWORDS TNF-R gene; tumor necrosis factor receptor 1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2161)
AUTHORS Nopar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zhang,R.,
 Aderka,D., Holtmann,H. and Wallach,D.

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TITLE Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
for the type I TNF-R, cloned using amino acid sequence data of its
soluble form, encodes both the cell surface and a soluble form of
the receptor.
JOURNAL EMBO J. 9 (10), 3269-3278 (1990)
MEDLINE 91006021
PUBMED 1698610
FEATURES
source Location/Qualifiers
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BASE COUNT 459 a 642 c 604 g 456 t
ORIGIN
Query Match 99.9%; Score 1366.4; DB 9; Length 2161;
Best Local Similarity 99.9%; Pred. No. 2,1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ATGGGCTCTCCACCGCTGCTGACCTGCTGCTGCCATGCTGTGCTGAGCTGTTGCTG 60
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QY 421 TTCAGTGTCTCAATGTCAGACCTCTGCTCAATGAGACCGTGCACCTCTCTGCGCAGAG 480
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Db 736 AAACAGAACACCGTGTGACCTGTCATGCAAGTTTCTTTCTAAGAGAAACAGAGTGTCTC 795
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Db 796 TCCGTGTAACTGTAGAGAAAGCCGTGAGTGCACGAAAGTTGGCCCAACCCAGATTGAG 855
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Db 916 GGTCTTGGCCCTTTTATCCCT 975
QY 721 TCCAGGCTCTACTCATTTGTTTGGGAAATGCAACACCTGTAAAGAGGGGAGCTTGA 780
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Db 976 TCCAGGCTCTACTCATTTGTTTGGGAAATGCAACACCTGTAAAGAGGGGAGCTTGA 1035
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Db 1576 CTTTGGGCGCCCGCGGCTTCCCGCGCGCGCGCAAGTCTTCTCAGATGA 1623

RESULT 10

LOCUS A43873 2175 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 1 from Patent EP0657536.
ACCESSION A43873
VERSION A43873.1 GI:2299022
KEYWORDS
SOURCE unidentified.

ORGANISM unidentified
REFERENCE unclassified.
AUTHORS 1 (bases 1 to 2175)
TITLE Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
JOURNAL Proteases capable of shedding the soluble TNF-receptor and TNF-R
derived peptides and antibodies against the proteases inhibiting
the shedding
Patent: EP 0657536-A 1 14-JUN-1995;
YEDA RES & DEV (IL)
COMMENT Other publication ZA 9407962 951121
Other publication JP 7194376 950801
Other publication AU 7574294 950504
Other publication CA 2133872 950413.
location/Qualifiers
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PSILR"
BASE COUNT 474 a 641 c 604 g 456 t
ORIGIN
Query Match 99.9%; Score 1366.4; DB 6; Length 2175;
Best Local Similarity 99.9%; Pred. No.2,1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
QY 1 ATGGGCTGCTCCACCGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
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Db	1336	GCCGATGGAGAACGTGGCCCCCTTGGCGTGGAAAGAAATTCGTGCGGCGCCTTAGGGCTG	1395
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OY	1321	CTTTCGGGCGCCCGCGCCCTCCCGCGCGCCGACGTCCTTCAGATGA	1368
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DEFINITION	Sequence 7 from Patent EP0568925.		
ACCESSION	A78738		
VERSION	A78738.1	GI:6090341	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 2175)		
AUTHORS	Brakebusch,C. and Wallach,D.		
TITLE	TNF RECEPTOR ACTION MODULATION		
JOURNAL	Patent: EP 0568925-A 7 10-NOV-1993;		
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841	CCACACCTTGAGCTTCAAGTCCCGTGGCCCAAGTTCACCTTCACTCAGCTTCAACCTATAC 900
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VERSION	AR041076.1	GI:5961572			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2175) Wallach,D., Nopnar,Y., Kemper,O., Engelmann,H., Brakbusch,C. and Aderka,D.				
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JOURNAL	Patent: US 5811261-A 1 22-SEP-1998;				
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Query Match	99.9%: Score 1366.4; DB 6; Length 2175;				
Best Local Similarity	99.9%: Pred. No. 2,1e-265;				
Matches 1367; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
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OY 181	AAGGCCCAAGAGAACTACTTGTACAAATGACGTCCAGGCCCGGGGACAGATACGGAC 240				
Db 436	AAGGCCCAAGAGAACTACTTGTACAAATGACGTCCAGGCCCGGGGACAGATACGGAC 495				

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Db	556	AGCTCTCTCAAAATCCCGAAGAAGAAATGGGTCAAGTGGAGATCTCTTCTTGACACAGTGAC	615
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Oy 421 TTCCAGTCTTCATTTGGACGCTCTGCCTCAATGGGACCGTGCACCTCTCTGCGAGAG 480
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2002, 19:18:10 ; Search time 2059 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1076)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
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Location/Qualifiers 1..1076

FEATURES
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/lab.host="DH10B"
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female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb.
Insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

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ORIGIN
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Best Local Similarity 99.4%; Pred. No. 2.1e-189;
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Db 554 AAGGTGCCCCGTTGGCTGCGTGAAGAAATTCGTGCGGCGCTAGGGCTGAGCGACGAG 613

QY 1153 ATCGATCGGCTGAGCTGAGAGAGGGGGCTGCTGCGGAGGCGGCAATACAGCATGCG 1212
    |||||||
Db 614 ATCGATCGGCTGAGCTGAGAGAGGGGGCTGCTGCGGAGGCGGCAATACAGCATGCG 673

QY 1213 GCGACCTGAGAGGCGGCGACGCGCGCGGCGAGCCAGCTGAGTGTGAGGACGCGTG 1272
    |||||||
Db 674 GCGACCTGAGAGGCGGCGACGCGCGCGGCGAGCCAGCTGAGTGTGAGGACGCGTG 733

QY 1273 CTCGCGGACATGAGACTGCTGGGCTGCTGAGAGACATCGAGAGGGCGCTTTGCGGCGCC 1332
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Db 734 CTCGCGGACATGAGACTGCTGGGCTGCGCTGAGAGACATCGAGAGGCCCTTTGNGCCGCC 793
QY 1333 GCGGCGCTCCCGCGCGCGGCGGCGAGCTCTTCAGATGA 1368
    |||||||
Db 794 GNGCGCTTCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 829

RESULT 2
LOCUS      B0723672
DEFINITION AGENCOURT_8489850_lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6184295 5', mRNA sequence.
ACCESSION  B0723672
VERSION    B0723672.1
KEYWORDS   GI:21862569
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 931)
            NIH-MGC http://mgc.ncl.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
AUTHORS    Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            CDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13573 row: d column: 24
            High quality sequence stop: 607.
FEATURES
    source          location/Qualifiers
    1..931
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:6184295"
    /clone.lib="lupski_dorsal_root_ganglion"
    /sex="male"
    /tissue_type="dorsal root ganglia"
    /dev_stage="adult, 36 yr"
    /lab_host="DH10B"
    /Note="Vector: PCMV-SpOrf6 (Life Technologies); Site_1:
    NotI; Site_2: SalI; cDNA made by oligo-dT priming.
    directionally cloned using the following adaptors:
    5'-TCGACCCAGCGCTCCG-3' and
    5'-GACTAGTCTAGATCGGAGCGGCGGCGGCGGCT(15)-3'. Size selected >
    1 kb for average insert length 1.7 kb. This is a primary
    library, non-amplified. Library constructed by Life
    Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
    College of Medicine) and is available through Life
    Technologies."

BASE COUNT      218 a      283 c      224 g      204 t      2 others
ORIGIN
Query Match      58.7%; Score 803.6; DB 14; Length 931;
Best Local Similarity 95.0%; Pred. No. 7e-188;
Matches 862; Conservative 0; Mismatches 40; Indels 5; Gaps 3;

QY 111 GGAGAAGAGATGATGTGTGCCCAAGAAATATATCCACCCCTCAAAATATTCGAT 170
    |||||||
Db 1 GGAGAAGAGATGATGTGTGCCCAAGAAATATATCCACCCCTCAAAATATTCGAT 60

QY 171 TTGCTGTACCAAGTGCACAAAGAACCTACTTTGTACATGACTGTCCAGGCCCGGGGCA 230
    |||||||
Db 61 TTGCTGTACCAAGTGCACAAAGAACCTACTTTGTACATGACTGTCCAGGCCCGGGGCA 120

QY 231 GGATAGGAGTGCAGGAGATGTGAGAGCGGCTCTTACCGCTTACGAAACCACTCGAG 290
    |||||||
Db 121 GGATAGGAGTGCAGGAGATGTGAGAGCGGCTCTTACCGCTTACGAAACCACTCGAG 180

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QY	291	ACACGCGCTCAGGCTGCTCCAAATGCGGAAAGAAATGGGTGACGGTGGAGATCTCTTTG	350
Db	181	ACACTGCTCAGCTGCTCTCAAAATGCCGAAAGAAATGGGTGACGGTGGAGATCTCTTTG	240
QY	351	CACAGTGCACCGGGGACACCGCTGTGTGGGCTGCAGAGAAGAACAGTACCGGATATTATGGAG	410
Db	241	CACAGTGCACCGGGGACACCGCTGTGTGGGCTGCAGAGAAGAACAGTACCGGATATTATGGAG	300
QY	411	TGAAAACCTTTTCCAGTGCCTTCAATTTGCAGGCTCTGCCTCAATGGGACCGTGACCTCTC	470
Db	301	TGAAAACCTTTTCCAGTGCCTTCAATTTGCAGGCTCTGCCTCAATGGGACCGTGACCTCTC	360
QY	471	CTGCCAGAGAAACAGAAACACCGGTGTGCACCTGCCATGCAGGTTCTTTCTTAAGGAAA	530
Db	361	CTGCCAGAGAAACAGAAACACCGGTGTGCACCTGCCATGCAGGTTCTTTCTTAAGGAAA	420
QY	531	CGAGTGTCTTCCTTACTTAAGTGAAGAAAAGCTTGAGTGCAGAGTTGTGCTTACC	590
Db	421	CGAGTGTCTTCCTTACTTAAGTGAAGAAAAGCTTGAGTGCAGAGTTGTGCTTACC	480
QY	591	CCAGATTGAGATGTTAAGGGGCACTGAGAGACTCAGGACACACAGTGTGTGGCCCTGGT	650
Db	481	CCAGATTGAGATGTTAAGGGGCACTGAGAGACTCAGGACACACAGTGTGTGGCCCTGGT	540
QY	651	CATTTTCTTTGGTCTTGGCTTTTATCCCTCCTCTTCAATGGTTTAATGTATCGCTACCA	710
Db	541	CATTTTCTTTGGTCTTGGCTTTTATCCCTCCTCTTCAATGGTTTAATGTATCGCTACCA	600
QY	711	ACGGTGAAGTCCAAAGCTCTACTCCATTTGTTGTGGGAAATGCAGACCTGAAAGAGAGG	770
Db	601	ACGGTGAAGTCCAAAGCTCTACTCCATTTGTTGTGGGAAATGCAGACCTGAAAGAGAGG	660
QY	771	GGAGCTTGAAGGAACACTACTACTAAGCCCTGCGCCCAAAACCCAACTTCACTGCTCCACTCC	830
Db	661	GGAGCTTGAAGGAACACTACTACTAAGCCCTGCGCCCAAAACCCAACTTCACTGCTCCACTCC	720
QY	831	AGGCTTCAACCCCCACCCCTG-GGCTTCAAGTCCCGTGCACAGTTCCACTTACCTCCAGCT	889
Db	721	AGGCTTCAACCCCCACCCCTGNNCGTTCAGTCTCCGTCGCCAGTTCCACTTACCTCCAGCT	780
QY	889	CCACCTTAA-CCCCGGGTGAGTGTCCCAACTTTGGG---CTCCCCGAGAGAGGTGGGA	945
Db	781	CCACCTTAA-CCCCGGGTGAGTGTCCCAACTTTGGGCTCCCCGAGAGAGGTGGGACC	840
QY	946	CCACCTTCAAGGGGGGCTGAGCCCATCTCTTGGAGACGCTTGCCTCGACCCCATCTCCC	1005
Db	841	CACCCCTTCAAGGGGGGCTGAGACCCCATCTCTTGGCGACAGGCCCTCCGCTCCGAGACC	900
QY	1006	AACCCCGC 1012	
Db	901	CATTCCC 907	
RESULT 3			
LOCUS	AL559050		
DEFINITION	AL559050 LTI_NFL008.TC2 Homo sapiens cDNA clone CS0D010YB05 5		
ACCESSION	AL559050		
VERSION	AL559050.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	1 (bases 1 to 957)		
AUTHORS	Ll.B., Gruber,C., Jesssee,J. and Polayes,D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001)		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	BP 191 91006 EVRY cedex - France		
	Email: sequele@genoscope.cns.fr, Web : www.genoscope.cns.fr.		

FEATURES	SOURCE	Location/Qualifiers
		1..957
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="CS0DJ010YB05"
		/clone_lib="LRI_NFL008_Tc2"
		/sex="male"
		/tissue_type="T cells from T cell leukemia"
		/note="(vector: pCMVSport 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(47) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSport 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Ling Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT	222 a	262 c 252 g 220 t 1 others
ORIGIN		

	Query Match	55.9%	Score 764.6;	DB: 9;	Length 957;	
	Best Local Similarity	99.9%	Pred. No. 3e-178;			
	Matches 764;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1	ATGGGCGCTTCACACCGTGCCTGCCTGCCTGCGCCACTGCGTCTCCTGAGCTGTGGTG	60			
Db	193	ATGGGCGCTTCACACCGTGCCTGCCTGCCTGCGCCACTGCGTCTCCTGAGCTGTGGTG	252			
OY	61	GGAAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAAGGGACAGGAAGA	120			
Db	253	GGAAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAAGGGACAGGAAGA	312			
OY	121	GATATGTGTGCCCAAGAAAATAATATCCACCCTCAAATTAATTCGATTGGCTGAC	180			
Db	313	GATATGTGTGTGCCCAAGAAAATAATATCCACCCTCAAATTAATTCGATTGGCTGAC	372			
OY	181	AAGTCCCAAAAGAACCTACTTGTACATGACTGCCAGGCCGAGGAGATACGAG	240			
Db	373	AAGTCCCAAAAGAACCTACTTGTACATGACTGCCAGGCCGAGGAGATACGAG	432			
OY	241	TGCAGGAGTGTGAGAGCGGCTCCTTCACCCGTTGAGAAAAACACCTCAGACACTGCTC	300			
Db	433	TGCAGGAGTGTGAGAGCGGCTCCTTCACCCGTTGAGAAAAACACCTCAGACACTGCTC	492			
OY	301	AGCTCTCCAAATGGCGAAAGAAATGGGTGACGGTAGATCTCTTTCGACACTGGAC	360			
Db	493	AGCTCTCCAAATGGCGAAAGAAATGGGTGACGGGTAGATCTCTTTCGACACTGGAC	552			
OY	361	CGGGACACCGTGTGTGCGTGCAGAGAAACAGTACCGGCAATTATTGGAGTGAACA	420			
Db	553	CGGGACACCGTGTGTGCGTGCAGAGAAACAGTACCGGCAATTATTGGAGTGAACA	612			
OY	421	TTTCAGTGCCTCAATTGACAGCCTGTGCCTCAATGGGACGTGCACCTCTCCTGCCAGAG	480			
Db	613	TTTCAGTGCCTCAATTGACAGCCTGTGCCTCAATGGGACGTGCACCTCTCCTGCCAGAG	672			
OY	481	AAACGAAACACCGTGTGACACCTGCATCAGGTTCTTTTAAGAGAAAACAGAGTGTG	540			
Db	673	AAACGAAACACCGTGTGACACCTGCATCAGGTTCTTTTAAGAGAAAACAGAGTGTG	732			
OY	541	TCTCTAGTAACTGTAAAGAAAAAGCCTGAGAGTGCACGAAGTTGTGACTACCCAGATTGAG	600			
Db	733	TCTCTAGTAACTGTAAAGAAAAAGCCTGAGAGTGCACGAAGTTGTGACTACCCAGATTGAG	792			
OY	601	AATGTTAAGGCGACTGAGAGACTCAGGACACACAGTGTGTGCCCCCTGTCTATTTTCTTT	660			
Db	793	AATGTTAAGGCGACTGAGAGACTCAGGACACACAGTGTGTGCCCCCTGTCTATTTTCTTT	852			
OY	661	GGTCTTTGGCTTTTATCCCTCCTCTTCATAGGTTAAATGTAATCGTTACCAACGGGAG	720			
Db	853	GGTCTTTGGCTTTTATCCCTCCTCTTCATAGGTTAAATGTAATCGTTACCAACGGGAG	912			

QY 721 TCACAGCTCTACTCATTTGTTGGGAAATGACACCTGAAAA 765
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Db 913 TCACAGCTCTACTCATTTGTTGGGAAATGACACCTGAAAA 957
RESULT 4
LOCUS B1860918 741 bp mRNA linear EST 10-OCT-2001
DEFINITION 60330284F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5399108 5',
mRNA sequence.
ACCESSION B1860918
VERSION B1860918.1 GI:16001653
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 741)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM12017 row: h column: 21
High quality sequence stop: 740.
location/Qualifiers
1. 741
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5399108"
/clone_lib="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; 0.190-0.7 primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 167 a 229 c 175 g 170 t
ORIGIN

Query Match 51.4%; Score 703.6; DB 13; Length 741;
Best Local Similarity 98.5%; Pred. No. 3.5e-163;
Matches 731; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

QY 257 GCGGCTCTTACCGCTTCAGAAAAACCACTGACACTGCTGCTCCAAATGCC 316
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Db 1 GCGGCTCTTACCGCTTCAGAAAAACCACTGACACTGCTGCTCCAAATGCC 60
QY 317 GAAAGAAATGGGTGAGTGGAGATCTCTCTGACAGTGGACGGGACACCGTGTG 376
|||||
Db 61 GAAAGAAATGGGTGAGTGGAGATCTCTCTGACAGTGGACGGGACACCGTGTG 120
QY 377 GCTGACAGAAACCACTACCGGATATTGAGTGAATGAACTTTTCCAGTGTCAATT 436
|||||
Db 121 GCTGACAGAAACCACTACCGGATATTGAGTGAATGAACTTTTCCAGTGTCAATT 180
QY 437 GCAGCTCTGCTCAATGAGGACGCTGCTCTGCTCCAGAGAGAAACAGAACCGTGT 496
|||||
Db 181 GCAGCTCTGCTCAATGAGGACGCTGCTCTGCTCCAGAGAGAAACAGAACCGTGT 240
QY 497 GCAGCTCTGCTCAATGAGGATTTTCTAGAGAAAAAGAGTGTCTCTGAGTAACTGTA 556
|||||
Db 241 GCAGCTCTGCTCAATGAGGATTTTCTAGAGAAAAAGAGTGTCTCTGAGTAACTGTA 300
QY 557 AGAAAGCTGTGAGTGCAGCAAGTTGTCTACCCAGATGAGAAATGTTAAGGGCACTG 616

Db 301 AGAAAGCTGTGAGTGCAGCAAGTTGTCTACCCAGATGAGAAATGTTAAGGGCACTG 360
QY 617 AGAGCTAGAGCAGACAGTGTGCTGGCCCTGGCTCATTTTCTTGGCTTTCCTTTTAT 676
|||||
Db 361 AGAGCTAGAGCAGACAGTGTGCTGGCCCTGGCTCATTTTCTTGGCTTTCCTTTTAT 420
QY 677 CCCCTCTTCATTTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 736
|||||
Db 421 CCCCTCTTCATTTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 737 TTGTTTGTGGAAATGACACCTGAAAAAGAGGGGAGCTTGAAGAACTACTACTAAGC 796
|||||
Db 481 TTGTTTGTGGAAATGACACCTGAAAAAGAGGGGAGCTTGAAGAACTACTACTAAGC 540
QY 797 CCCCGGCCCCAAACCCAGCTTCAGTCCCTCCAGCTTCACCCGCTTACCCGCTGCTCA 856
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Db 541 CCCCGGCCCCAAACCCAGCTTCAGTCCCTCCAGCTTCACCCGCTTACCCGCTGCTCA 600
QY 857 GTCCCGTGGCCAGTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTC 916
|||||
Db 601 GTCCCGTGGCCAGTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTC 660
QY 917 ACTTTGGGGCTCCCGGAGAGAGGTGGACACCTATCA-GGGGCTGACCCCATCTT 975
|||||
Db 661 ACTTTGGGGCTCCCGGAGAGAGGTGGACACCTATCAAGGGGGCTGACCCCATCTT 719
QY 976 GCGACACCTCTCGCTCCGAC 997
|||||
Db 720 GCGACACCTCTCGCTCCGAC 741
RESULT 5
LOCUS AU117362 889 bp mRNA linear EST 01-AUG-2002
DEFINITION AU117362 HEMBA1 Homo sapiens cDNA clone HEMBA1001229 5', mRNA
sequence.
ACCESSION AU117362
VERSION AU117362.1 GI:10932324
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 889)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Salto,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
location/Qualifiers
1. 889
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1001229"
/clone_lib="HEMBA1"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/note="Vector: pME18F13"
BASE COUNT 167 a 301 c 249 g 166 t 6 others
ORIGIN

Query Match 50.4%; Score 689; DB 9; Length 889;
Best Local Similarity 99.4%; Pred. No. 1.5e-159;
Matches 700; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 665 TTGGCTTTATCCCTCTCTTCATTTGTTAATGTATCGTACCAACGGTGAAGTCCA 724
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Db 1 TTGGCTTTATCCCTCTCTTCATTTGTTAATGTATCGTACCAACGGTGAAGTCCA 60
OY 725 AGCTTACTCATTTGTTGGGAATGACACCTGAAAGAGGGAGCTTGAAGAA 784
|||||
Db 61 AGCTTACTCATTTGTTGGGAATGACACCTGAAAGAGGGAGCTTGAAGAA 120
OY 785 CTACTACTAAGCCCTGGCCCAACCAAGCTTCACTCCACTCAGGCTTCAACCCCA 844
|||||
Db 121 CTACTACTAAGCCCTGGCCCAACCAAGCTTCACTCCACTCAGGCTTCAACCCCA 180
OY 845 CCCTGGGCTTCACTCCCTGCTCCCACTTCCACTTCACTCAGCTTCACTTACCCCG 904
|||||
Db 181 CCCTGGGCTTCACTCCCTGCTCCCACTTCCACTTCACTCAGCTTCACTTACCCCG 240
OY 905 GTGACTGTCCCAACTTGGGGCTCCCGGAGAGAGTGGACACCACTATCAAGGGGGCTG 964
|||||
Db 241 GTGACTGTCCCAACTTGGGGCTCCCGGAGAGAGTGGACACCACTATCAAGGGGGCTG 300
OY 965 ACCCATCTTGGCGACAGCCCTCGCTCGACCCCATCCCAACCCCTTCAAGAGTGGG 1024
|||||
Db 301 ACCCATCTTGGCGACAGCCCTCGCTCGACCCCATCCCAACCCCTTCAAGAGTGGG 360
OY 1025 AGGACAGCGCCCAAGCCACAGACCTAGACACTGATGACCCCGCGAGCTTACGGCG 1084
|||||
Db 361 AGGACAGCGCCCAAGCCACAGACCTAGACACTGATGACCCCGCGAGCTTACGGCG 420
OY 1085 TGGTGGAAAGTGGCCCCCTTGGCGCTGGAAGGAATTTGGGGGGCTTACGGGCTGACG 1144
|||||
Db 421 TGGTGGAAAGTGGCCCCCTTGGCGCTGGAAGGAATTTGGGGGGCTTACGGGCTGACG 480
OY 1145 ACCAGAGATCGATCGGCTGAGCTGAGAAAGGGCGCTGCTGGCGAGCGCAATACA 1204
|||||
Db 481 ACCAGAGATCGATCGGCTGAGCTGAGAAAGGGCGCTGCTGGCGAGCGCAATACA 540
OY 1205 GCATCTGGCGACCTGAGAGGGGGCGACCGCGCGCGAGGCGACGCTGAGCTGTGG 1264
|||||
Db 541 GCATCTGGCGACCTGAGAGGGGGCGACCGCGCGCGAGGCGACGCTGAGCTGTGG 600
OY 1265 GACGGTCTCCGGACATGACCTGCTGGCTGAGAGACATTCAGAGAGGGGCTTT 1324
|||||
Db 601 GACGGTCTCCGGACATGACCTGCTGGCTGAGAGACATTCAGAGAGGGGCTTT 660
OY 1325 GCGGCGCGCGCCCTCCCGCGCGCGCCAGCTTCTCAGATGA 1368
|||||
Db 661 GCGGCGCGCGCG - CCTCCGCGCGCGCCAGCTTCTCAGATGA 703

RESULT 6
AUI31978 761 bp mRNA linear EST 01-AUG-2002
LOCUS AUI31978 NT2RP3 Homo sapiens cDNA clone NT2RP300370 5', mRNA
DEFINITION AUI31978 NT2RP3 Homo sapiens cDNA clone NT2RP300370 5', mRNA
sequence.
ACCESSION AUI31978
VERSION AUI31978.1 GI:10992332
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 761)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Makamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isogai, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory

Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. 761
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP300370"
/clone_1bp="NT2RP3"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18FL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT 178 a 199 c 201 g 179 t 4 others
ORIGIN

Query Match 49.9%; Score 682.4; DB 9; Length 761;
Best Local Similarity 99.1%; Pred. No. 6.1e-158;
Matches 694; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 1 ATGGGCTCTCTCCACCGTCCCTGACCTGCTGCTGCACACTGCTCTCTGAGACTGTGGTG 60
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Db 62 ATGGGCTCTCTCCACCGTCCCTGACCTGCTGCTGCACACTGCTCTCTGAGACTGTGGTG 121
OY 61 GGAATATACCCCTCGAGGGGTTATTGGACTGGTCCCTCACTAGGGGACAGGAGAGA 120
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Db 122 GGAATATACCCCTCGAGGGGTTATTGGACTGGTCCCTCACTAGGGGACAGGAGAGA 181
OY 121 GATAGTGTGTCTCCCAAGAAATATATCAACCTCAAAATTAATTCGATTTGCTGTAC 180
|||||
Db 182 GATAGTGTGTCTCCCAAGAAATATATCAACCTCAAAATTAATTCGATTTGCTGTAC 241
OY 181 AAGTCCCAAAAGAAAGAACTACTTGTACAAATGACTTCCAGGCGCGGGGACAGATACGAG 240
|||||
Db 242 AAGTCCCAAAAGAAAGAACTACTTGTACAAATGACTTCCAGGCGCGGGGACAGATACGAG 301
OY 241 TGCAGGAGTGTGAGAGGGGCTCTCTTCAACCGCTTCAAGAAACCACTCAGACACTGCTC 300
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Db 302 TGCAGGAGTGTGAGAGGGGCTCTCTTCAACCGCTTCAAGAAACCACTCAGACACTGCTC 361
OY 301 AGCTGCTCCAAATGCGGAAGAAATGGGTGAGTGAATCTCTTCTTGCACACTGGAC 360
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Db 362 AGCTGCTCCAAATGCGGAAGAAATGGGTGAGTGAATCTCTTCTTGCACACTGGAC 421
OY 361 CGGACACCGTGTGTGGCTGAGAGAAACAGTACCGGCATTAATGAGTGAAGAAACCTT 420
|||||
Db 422 CGGACACCGTGTGTGGCTGAGAGAAACAGTACCGGCATTAATGAGTGAAGAAACCTT 481
OY 421 TTCCAGTCTTCAATTTGACGCTTGCCTCAATGGGAGCGTGCACCTCTCCGACAGAG 480
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Db 482 TTCCAGTCTTCAATTTGACGCTTGCCTCAATGGGAGCGTGCACCTCTCCGACAGAG 541
OY 481 AAACAGAACACCGTGTGACACCTGCCATGAGGTTCTTTCTTAAGAGAAACGAGTGTGC 540
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Db 542 AAACAGAACACCGTGTGACACCTGCCATGAGGTTCTTTCTTAAGAGAAACGAGTGTGC 601
OY 541 TCCTGTACTACTGTAAAGAAAGCTTGAAGTGCACGAAGTGTGCTTACCCAGATTGAG 600
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Db 602 TNCGTACTACTGTAAAGAAAGCTTGAAGTGCACGAAGTGTGCTTACCCAGATTGAG 661
OY 601 AATGTTAAGGACACTGAGAGACTCAGGACACACAGTGC-TGTTGCCCTGCTCATTTTCTT 659
|||||
Db 662 AATGTTAAGGACACTGAGAGACTCAGGACACACAAATGCTTGTGCCCTGACATTTTCTT 721
OY 660 TGGTCTTGGCTTTTATCCCTCTCTTCATTTGATTGAG 699
|||||
Db 722 TGGTCTTGGCTTTTATCCCTCTCTTCATTTGATTGAG 761

LOCUS	AL529836	942 bp	mRNA	linear	EST 13-FEB-2001
DEFINITION	AL529836 LTR1.NFL001.NBC4		Homo sapiens	CDNA clone	CSDD005YP05 5
ACCESSION	AL529836		prime, mRNA sequence.		
VERSION	AL529836.1	GI:12793329			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 942)				
TITLE	Li, W.B., Gruber, C., Jesssee, J., and Polayes, D.				
JOURNAL	Full-length cDNA libraries and normalization unpublished (2001)				
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.				
FEATURES	Source				
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	/db_xref="taxon:9606"				
	/clone="CSDD005YP05"				
	/clone_1lb="LTR1.NFL001.NBC4"				
	/sex="male"				
	/tissue_type="neuroblastoma cells"				
	/lab_host="DH10B"				
	/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9600 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"				
BASE COUNT	208 a 259 c 248 g 224 t				3 others
ORIGIN					
Query Match	49.7%;	Score 680;	DB 9;	Length 942;	
Best Local Similarity	99.0%;	Prod. No. 2.5e-15;			
Matches 703;	Conservative 12;	Mismatches 3;	Indels 2;	Gaps 2;	
OY	1	ATGGGCTCTCCACCGCTGACCTGCTGCGTGCACCTGATGGTCTCTGAGCTGTGGG	60		
DB	234	ATGGGCTCTCTCCACCGCTGACCTGCTGCTGCTGCGTGTGCTCTCTGAGCTGTGGG	293		
OY	61	GGAATATACCCCTCAGGGGTTATTGACTGTCCCTCACTAAGGGACAGGAGAAGA	120		
DB	294	GGAATATACCCCTCAGGGGTTATTGACTGTCCCTCACTAAGGGACAGGAGAAGA	353		
OY	121	GATAGTGTGTGCCCCCAAGAAATATATCCACCTCAAAATTAATTCATTGCTGTACC	180		
DB	354	GATAGTGTGTGCCCCCAAGAAATATATCCACCTCAAAATTAATTCATTGCTGTACC	413		
OY	181	AAGTCCCAAGAAAGAACTACTTGTACATGACTTCCAGGCGCGGGCAGAGATCGGAC	240		
DB	414	AAGTCCCAAGAAAGAACTACTTGTACATGACTTCCAGGCGCGGGCAGAGATCGGAC	473		
OY	241	TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAGAAAAACACACTGACCTGCCTC	300		
DB	474	TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAGAAAAACACACTGACCTGCCTC	533		
OY	301	AGCTCTCCAAATGCGGAAAGAAATGGGTGAGGTGAGATCTCTTTCGACAGTGGAC	360		
DB	534	AGCTCTCCAAATGCGGAAAGAAATGGGTGAGGTGAGATCTCTTTCGACAGTGGAC	593		
OY	361	CGGACACACGCTGTGCTGTCAGAGAAGAACAGTACCGGCAATTATTGGATGAAACCTT	420		

Db	594	CGGAGACCGCTGTGGCGTGCAGGAAGAACCGTACCGGCATTTGGAGTGAACACCT	653
QY	421	TTTCAGATGCTTAAATTGCAGGCTCTGCTCAATTGGAGCCGTGCACCTCTCTGCCAGAG	480
Db	654	TTCCAGATGCTTAAATTGCAGGCTCTGCTCAATTGGAGCCGTGCACCTCTCTGCCAGAG	713
QY	481	AAACAGAACACCGCTGGACCTGCATGAGG-TTCTCTTCTTAAGAGAAAGACGTGTGT	539
Db	714	AAACAGAACACCGCTGGACCTGCATGAGG-TTCTCTTCTTAAGAGAAAGACGTGTGT	773
QY	540	CTCTGCTAGTAACTGTAAAGAAAAGCTTGGATGCAGAAATTGTCTTACCCAGATTGA	599
Db	774	CTCTGCTAGTAACTGTAAAGAAAAGCTTGGATGCAGAAATTGTCTTACCCAGATTGA	832
QY	600	GAATGTTAAGGGACCTGAGAGACTGACGACCAACAGTGTGCCCCGTGTCATTTCCT	659
Db	833	GAATGTTAAGGGACCTGAGAGACTGACGACCAACAGTGTGCCCCGTGTCATTTCCT	892
QY	660	TGCTGCTTGTATCCCTCTTCTTCAATGTTGTTAATGATTCGCTAC	709
Db	893	TGCTGCTGTCCTTTATTCCTCTCTCTTCAATGTTAATGATTCGCTAC	942
RESULT 8			
LOCUS	BM546826	1070 bp	EST 20-FEB-2002
DEFINITION	AGENCOURT 6491128 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723557		
ACCESSION	BM546826		
VERSION	BM546826.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/.		
JOURNAL	National Institutes of Health. Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML) DNA Sequencing by: Agencourt Bioscience Corporation cDNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at: http://image.lnl.gov Plate: LML12711 row: g column: 14 High quality sequence start: 2 High quality sequence stop: 669. Location/Qualifiers 1..1070 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5723557" /clone_1lb="NIH_MGC_125" /lab_host="DH10B" /note="Organ: ovary (pool of 3); Vector: PCMV-SPORT6; site:1: EcoRV (destroyed); site:2: NotI; RNA source pool of 49 yo. library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."		
FEATURES	source		
BASE COUNT	241 a	311 c	293 g
ORIGIN			224 t
			1 others
Query Match	49.7%	Score 679.8;	DB 13; Length 1070;
Best Local Similarity	94.0%;	Pred. No. 2.8e-157;	

Matches 741: Conservative 0: Mismatches 38: Indels 9: Gaps 3:

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Db	206	ATGGGCGCTCTCCACCGCTGCTGACCTGCGTGCACAGTGGTCTCTGAGCTGTGGTG	265
OY	61	GGAATATACCCCTCAGGGGTTATTGGACTGTCTCTCAACCTTGGGGACAGGAGAAGA	120
Db	266	GGAATATACCCCTCAGGGGTTATTGGACTGTCTCTCAACCTTGGGGACAGGAGAAGA	325
OY	121	GATGAGTGTGTGCTCCCAAGAAATATATATACACCTCAAAATATATTCATTTGCTGTACC	180
Db	326	GATGAGTGTGTGCTCCCAAGAAATATATATACACCTCAAAATATATTCATTTGCTGTACC	385
OY	181	AAGTGGCACAAGGAACCTTGTATACATGACTGTCCAGGCGCGGGAGAGATACGGAC	240
Db	386	AAGTGGCACAAGGAACCTTGTATACATGACTGTCCAGGCGCGGGAGAGATACGGAC	445
OY	241	TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAAGAAACACCTCAGACACTGCTTC	300
Db	446	TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAAGAAACACCTCAGACACTGCTTC	505
OY	301	ACCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGGAGATCTCTTCTTGCACAGTGAC	360
Db	506	ACCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGGAGATCTCTTCTTGCACAGTGAC	565
OY	361	CGGGACACCGTGTGGTGGTGCAGAAACCACTACCGGATATTTGGATGAAACCTT	420
Db	566	CGGGACACCGTGTGGTGGTGCAGAAACCACTACCGGATATTTGGATGAAACCTT	625
OY	421	TTCCAGTGTCTCAATTTGACAGCTGTGCTCAATGGGACGCTGACCTCTCTGCCAGAG	480
Db	626	TTCCAGTGTCTCAATTTGACAGCTGTGCTCAATGGGACGCTGACCTCTCTGCCAGAG	685
OY	481	AAACAGAACACCGTGTGACAGCTGCTCAATGGGACGCTGACCTCTCTGCCAGAG	540
Db	686	AAACAGAACACCGTGTGACAGCTGCTCAATGGGACGCTGACCTCTCTGCCAGAG	745
OY	541	TCCTGTAGTACTGTAAAGAAACCGGAGTGCAGCAATTTGGCTTACCCAGATTTAG	600
Db	746	TCCTGTAGTACTGTAAAGAAACCGGAGTGCAGCAATTTGGCTTACCCAGATTTAG	805
OY	601	AATGTTAAGGACAGTGAAGTCAAGCAGACAGTGTGTTG-CCCTGCTCATTTTCTT	659
Db	806	AATGTTAAGGACAGTGAAGTCAAGCAGACAGTGTGTTG-CCCTGCTCATTTTCTT	865
OY	660	TGCTCTTTGCTTTTATTCCTCTCTTCAATGGGTTAATGATGCTGTACCAAC--GTTGG	717
Db	866	TGCTCTTTGCTTTTATTCCTCTCTTCAATGGGTTAATGATGCTGTACCAAC--GTTGG	925
OY	718	AAGTCCAAAG-----CTTACTGCAATGTTTGTGGAAATCGACACCTGAAAAAGGGGG	771
Db	926	AAGTCCAAAGCTCTTACTGCAATGTTTGTGGAAATCGACACCTGAAAAAGGGGG	985
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RESULT 9
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LOCUS AL577008 975 bp mRNA linear EST 16-FEB-2001
DEFINITION LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1082YA01 5
ACCESSION AL577008
VERSION AL577008.1 GI:12939716
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 975)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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BASE COUNT	231 a	258 c	259 g	221 t	6 others
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Query Match	49.6%	Score 678.2:	DB 9:	Length 975:	
Best Local Similarity	97.9%	Pred. NO. 6.9e-157:			
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Db	256	ATGGGCGCTCTCCACCGCTGCTGACCTGCGTGCACAGTGGTCTCTGAGCTGTGGTG	315		
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Db	436	AAGTGGCACAAGGAACCTTGTATACATGACTGTCCAGGCGCGGGAGAGATACGGAC	495		
OY	241	TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAAGAAACACCTCAGACACTGCTTC	300		
Db	496	TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAAGAAACACCTCAGACACTGCTTC	555		
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Db	556	ACCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGGAGATCTCTTCTTGCACAGTGAC	615		
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Db	616	CGGGACACCGTGTGGTGGTGCAGAAACCACTACCGGATATTTGGATGAAACCTT	675		
OY	421	TTCCAGTGTCTCAATTTGACAGCTGTGCTCAATGGGACGCTGACCTCTCTGCCAGAG	480		
Db	676	TTCCAGTGTCTCAATTTGACAGCTGTGCTCAATGGGACGCTGACCTCTCTGCCAGAG	735		
OY	481	AAACAGAACACCGTGTGACAGCTGCTCAATGGGACGCTGACCTCTCTGCCAGAG	540		
Db	736	AAACAGAACACCGTGTGACAGCTGCTCAATGGGACGCTGACCTCTCTGCCAGAG	795		
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OY	600	GAATGTTAAGGCGACTGAGGACTCAGGACACCACTGCTGTGCCCCGTGCTATTTTCTT	659		
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QY	660	TGCTGTTGACCTTATATCCCTCTCTTCAATGCTTAAATGATGCTTACCAAGGTTGG	718
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DEFINITION	K-EST001556 S6SNU620 Homo sapiens CDNA clone S6SNU620-5-C12 5',		
ACCESSION	BM742388		
VERSION	BM742388.1	GI:19063703	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 669) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.		
TITLE	21C Frontier Korean EST project 2001		
JOURNAL	unpublished (2002)		
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 5 row: C column: 12 High quality sequence stop: 669. Location/Qualifiers 1. 669 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="S6SNU620-5-C12" /clone_1lp="S6SNU620" /sex="F" /tissue_type="Ascites" /cell_type="Scattering floating" /cell_line="SNU-620" /lab_host="Top10F/" /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."		
FEATURES	source		
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Query Match	48.9%	Score 669;	DB 14; Length 669;
Best Local Similarity	100.0%	Pred. No. 1,2e-154;	
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QY	748	AAATGACACCTGAAAAAGAGGGGAGCTTGAAGGACTACTACTAAGCCCTGGCCCCA	807

Db	61	AAATGACACCTGAAAAAGAGGGGGAGCTTGAAGAAACTACTAAAGCCCTGGGCCCA	120
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Db	121	AAACCAAGCTTAGTCCCACTCCAGGCTTACACCCACCCTGGGCTTCACTCCGTGCC	180
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Db	181	AACTTCACCTTAGACCTCCAGCTCCACCTTATACCCCGGAGCTGCCAACTTTGGGGCT	240
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QY	1048	AGCCTAGACACTGATGACCCCGCGAGCGCTGATACGGCGGTGGAGAAAGTGCCCGCGTGG	1107
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QY	1108	CGCTGGAAGGAATTTGTGTGGGGCGCTAGAGGCTGAGAGACACAGATCATGCGCTGAGAG	1167
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QY	1168	CTGCAGAACGGGGCGCTGCTGCGGACAGGCGCAATACAGCATCTGGCGACCTGAGAGCGG	1227
Db	481	CTGCAGAACGGGGCGCTGCTGCGGACAGGCGCAATACAGCATCTGGCGACCTGAGAGCGG	540
QY	1228	CGCAGCGCGGGGGGGAGGGCCAGCGCTGAGAGCTGTGGAGCGGGTCTCCGGACAAATGGAC	1287
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QY	1288	CTGCTGGGCGTGGCTGAGAGACATCGAGAGAGCGCTTTGGCGCCCGCCCTCCCGGCC	1347
Db	601	CTGCTGGGCGTGGCTGAGAGACATCGAGAGAGCGCTTTGGCGCCCGCCCTCCCGGCC	660
QY	1348	GGCGCCCACT 1356	
Db	661	GGCGCCCACT 669	
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DEFINITION	60232676p1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5',		
ACCESSION	Bg180101		
VERSION	Bg180101.1	GI:12686804	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 974)		
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: DCTD/DP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov Plate: LMNL0185 row: 9 column: 20 High quality sequence stop: 657. Location/Qualifiers 1..974 /organism="Homo sapiens"		


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Qy 1018 AAGTGGAGGACAGCGCCACAGCCACAGAGCTAGACATGATGACCCCGGAGCGCTG 1077
Db 362 AAGTGGAGGACAGCGCCACAGCCACAGAGCTAGACATGATGACCCCGGAGCGCTG 421
Qy 1078 TACGCGCTGTGAGAAAGCTGCCCCGCTTGGCTGGAAGAAATTCGTGCGGCGCTAGAG 1137
Db 422 TACGCGCTGTGAGAAAGCTGCCCCGCTTGGCTGGAAGAAATTCGTGCGGCGCTAGAG 481
Qy 1138 CTGAGCGACACAGATGATGCTGAGCTGCAGAAAGGCGCTGCTTGGCGAGCG 1197
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RESULT 13

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LOCUS 718 bp mRNA linear EST 01-MAY-2001

DEFINITION 602626965F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751536 5',

mRNA sequence.

ACCESSION Bg680679

VERSION Bg680679.1 GI:13912076

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 718)

NIH-MGC <http://mgc.nci.nih.gov/>.

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLM10608 row: b column: 17

High quality sequence stop: 679.

Location/Qualifiers

1. 718

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/clone="IMAGE:4751536"

/clone_id="NCI_CGAP_Skn4"

/tissue_type="squamous cell carcinoma"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5kb. Library constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 134 a 254 c 198 g 132 t

ORIGIN

Query Match 48.8%; Score 667; DB 12; Length 718;

Best Local Similarity 96.4%; Pred. No. 3.8e-154;

Matches 684; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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Db 1 TTTCTTGGTGTGTTGCTTTATCCCTTCCTTATGTTTATGATGCTACCAAG 60
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Qy 774 GCTTGAAGAACTACTATAGCCCCCTGGCCCCCAACCAAGCTTCAGTCCATCCAG 833
Db 121 GCTTGAAGAACTACTATAGCCCCCTGGCCCCCAACCAAGCTTCAGTCCATCCAG 180
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Db 181 CTTCACCCCACTGCGCTTCACTCCGCTCCAGTTCCACTTCACTTCACCTCCAC 240
Qy 894 CTATACCCCGGTGACTGTGCCAACTTGGCGCTCCCGCAGAGAGGTGACACCTTA 953
Db 241 CTATACCCCGGTGACTGTGCCAACTTGGCGCTCCCGCAGAGAGGTGACACCTTA 300
Qy 954 TCAGGGGGCTGACCCCACTTGGGACAGCCCTGCGACCCCAATCCCAATCCCT 1013
Db 301 TCAGGGGGCTGACCCCACTTGGGACAGCCCTGCGACCCCAATCCCAATCCCT 360
Qy 1014 TCAGAAGTGGAGAGACAGCGCCCAAGCCACAGAGCTAGACCTATGACCCCGGAC 1073
Db 361 TCAGAAGTGGAGAGACAGCGCCCAAGCCACAGAGCTAGACCTATGACCCCGGAC 420
Qy 1074 GCTGTAGCCGCTGTGGAGAAAGTGCCTGCTGGAAGAAATTCGTGCGGCGCT 1133
Db 421 GCTGTAGCCGCTGTGGAGAAAGTGCCTGCTGGAAGAAATTCGTGCGGCGCT 480
Qy 1134 AGGCTGAGGACACACAGATGATGCGGCTGACATGAAACGGGGGCTGCTGCGGCGA 1193
Db 481 AGGCTGAGGACACACAGATGATGCGGCTGACATGAAACGGGGGCTGCTGCGGCGA 540
Qy 1194 GGCGCAATATACAGATGCTGGGACCTGGAGGCGGCGACCGCGGCGGACGCT 1253
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Qy 1313 AGGAGGGGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1347
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RESULT 14

BM800044

LOCUS 994 bp mRNA linear EST 05-MAR-2002

DEFINITION AGENCOURT_6415909 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531041

5', mRNA sequence.

ACCESSION BM800044

VERSION BM800044.1 GI:19116867

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 994)

NIH-MGC <http://mgc.nci.nih.gov/>.

Unpublished (1999)


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Db 498 AGCTGCTCCAAATGCCGAAAGAAATGGTTCAGGTGGAGATCTTCTTTCACAGTGGAC 557
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QY 421 TTCAGTCTTCAATTCAGAGCTCTGCTCAATGGGACGCTGCACCTTCCTGCCAGGAG 480
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QY 541 TCCTGTAGTAACTGTAAAGAAAGCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 600
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QY 601 AATGTTAAGGCACTGAGGACTCAGGACCAACAGTGTGT 640
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Search completed: December 4, 2002, 21:42:31
 Job time : 2087 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2002, 19:11:39 ; Search time 58 Seconds
(without alignments)
7233.342 Million cell updates/sec

Title: US-09-899-429A-1

Perfect score: 1368
Sequence: 1 atgggccttcaccctcaccgtgccc.....cgccacgtcttcacgatga 1368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1366.4	99.9	2161	US-09-106-038A-1	Sequence 1, Appl1
2	1366.4	99.9	2161	US-09-505-250-3	Sequence 3, Appl1
3	1366.4	99.9	2175	US-08-321-668-1	Sequence 1, Appl1
4	1366.4	99.9	2175	US-08-837-941-1	Sequence 1, Appl1
5	1366.4	99.9	2175	US-08-126-016-1	Sequence 1, Appl1
6	1366.4	99.9	2175	US-08-054-970-1	Sequence 1, Appl1
7	1360	99.4	2062	US-08-050-319B-24	Sequence 24, Appl1
8	1360	99.4	2062	US-08-465-982-24	Sequence 24, Appl1
9	690.4	50.5	1956	US-08-762-308-10	Sequence 10, Appl1
10	685.4	50.1	2440	US-09-513-007-1	Sequence 10, Appl1
11	632.8	46.3	6896	US-08-627-151A-6	Sequence 6, Appl1
12	632.4	46.2	6889	US-08-286-740-2	Sequence 2, Appl1
13	632.4	46.2	6889	PCR-US95-09576-2	Sequence 2, Appl1
14	593.6	43.4	600	US-08-050-319B-47	Sequence 47, Appl1
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16	515.4	37.7	1478	US-09-149-922-6	Sequence 6, Appl1
17	514	37.6	1301	US-08-804-166-7	Sequence 7, Appl1
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19	506	37.0	1147	US-08-804-166-5	Sequence 5, Appl1
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27	424.4	31.0	1049	US-08-910-991-1	Sequence 1, Appl1

28	424.4	31.0	1202	US-08-804-166-3	Sequence 3, Appl1
29	424.4	31.0	1202	US-08-910-991-3	Sequence 3, Appl1
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31	376.2	27.5	477	US-08-465-982-53	Sequence 53, Appl1
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36	337	24.6	427	US-09-397-787-236	Sequence 236, App
37	330	24.1	543	US-09-513-007-3	Sequence 3, Appl1
38	310.8	22.7	462	US-08-050-319B-51	Sequence 51, Appl1
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40	70	5.1	1634	US-08-928-069-11	Sequence 11, Appl1
41	70	5.1	1634	US-08-828-663A-9	Sequence 9, Appl1
42	70	5.1	1783	US-08-815-469-1	Sequence 1, Appl1
43	66.8	4.9	1234	US-08-815-469-3	Sequence 3, Appl1
44	53	3.9	7218	US-08-232-463-14	Sequence 14, Appl1
45	45	3.3	13987	US-08-804-227C-13	Sequence 13, Appl1

ALIGNMENTS

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RESULT 1
US-09-106-038A-1
; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-106-038A-1
;
Query Match          99.9%  Score 1366.4;  DB 3;  Length 2161;
Best Local Similarity 99.9%  Pred. No. 0;
Matches 1367;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Db 376 GATAGTGTGTCCCAAGAAATATATPCCACCTCAAAATTAATTCATTGTGTATCC 435
QY 181 AAGTGCCCAAGAAAGAACTTGTACAAATGCTGTCCAGGCCCGGGGAGATACGAG 240
Db 436 AAGTGCCCAAGAAAGAACTTGTACAAATGCTGTCCAGGCCCGGGGAGATACGAG 495
QY 241 TGGAGGGAGTGTGAGAGGGGCTCCCTACCGGCTTCAAGAAACCACTTACAGCTGCTC 300
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QY 301 AGCTGCTCCAAATCCCGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGACAGTGTGAC 360
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QY 421 TTCCAGTGCTTCAATGTGAGGCTGTGCTCAATGTGAGGACCGTGCACCTCTCTGCGAGAG 480
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QY 541 TCTGTAGTAACTGTAGAAAAAGCCTGAGTGCAGAGAAATTGTGCTTACCCAGATTGAG 600
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QY 601 AATGTAAAGGCACTGAGGACTGCAGGACCAACAGTGTGCTGCTGCTGCTGCTGCTGCTG 660
Db 856 AATGTAAAGGCACTGAGGACTGCAGGACCAACAGTGTGCTGCTGCTGCTGCTGCTGCTG 915
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QY 1321 CTTTGGGCGCGCGCGCGCTCCCGCGCGCGCGAGTCTTCAATGTA 1368
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RESULT 2

US-09-505-250-3

; Sequence 3, Application US/09505250A

; Patent No. 6329148

; GENERAL INFORMATION:

; APPLICANT: Rosen, Glenn

; APPLICANT: Kao, Peter

; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with

; TITLE OF INVENTION: Triptolides and Death Domain Ligands

; FILE REFERENCE: SUN-109PRV2

; CURRENT APPLICATION NUMBER: US/09/505,250A

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 2161

; TYPE: DNA

; ORGANISM: H. sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (256)...(1623)

US-09-505-250-3

Query Match 99.9%; Score 1366.4; DB 4; Length 2161;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 121 GATAGTGTGTGCTCCCAAGAAATATATPCCACCTCAAAATTAATTCATTGTGTATCC 180
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Db 436 AAGTGCCCAAGAAAGAACTTGTACAAATGCTGTCCAGGCCCGGGGAGATACGAG 495
QY 241 TGGAGGAGTGTGAGAGGCTGCTTCAACCGCTTCAAGAAACCACTTACAGACTGCTC 300
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QY 301 AGCTGCTCCAAATCCCGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGACAGTGTGAC 360
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QY 421 TTCCAGTGCTTCAATGTGAGGCTGTGCTCAATGTGAGGACCGTGCACCTCTCTGCGAGAG 480
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 QY 661 GGTCTTTGCTTTATCT 720
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 Db 976 TCCAGGCTTCACTCAATGTTTGTGGAAATCGACACCTGAAAAAGAGGGGAGCTTGAA 1035
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 Db 1096 CCCACCTGAGGCTTCACTCCGCTGCCCCAGTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 1155
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 Db 1216 GCTGACCCCAATCTGTTGGAGAGCCCTGCTCCGACCCCACTCCCACTCCCACTCCCACTCCCA 1275
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 Db 1576 CTTTGGGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1623

RESULT 4

US-08-837-941-1

; Sequence 1, Application US/08837941
 ; Patent No. 576917

; GENERAL INFORMATION:
 ; APPLICANT: WALLACH, David

; APPLICANT: BRAKEBUSCH, Cord
 ; APPLICANT: VAREJOMERY, Eugene

; APPLICANT: BARKIN, Michael
 ; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF

; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/837,941
 ; FILING DATE: 28-APR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/321,668
 ; FILING DATE: 12-OCT-1994
 ; APPLICATION NUMBER: IL 107268
 ; FILING DATE: 12-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: WALLACH-13
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2175 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 256..1620
 ; US-08-837-941-1

Query Match 99.9%; Score 1366.4; DB 1; Length 2175;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTCTTCACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
 Db 256 ATGGGCTCTTCACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
 QY 61 GGAATATACCCCTCAGGGGTTATTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 Db 316 GGAATATACCCCTCAGGGGTTATTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
 QY 121 GATAGTGTGTGTCGCCAAGAAATATATATCCACCTCAAAATATATGATTTGCTGTAC 180
 Db 376 GATAGTGTGTGTCGCCAAGAAATATATATCCACCTCAAAATATATGATTTGCTGTAC 435
 QY 181 AAGTGCACAAAGAACTTCTGTACATGACTGTGACAGGCGCGGAGAGATAGGAG 240
 Db 436 AAGTGCACAAAGAACTTCTGTACATGACTGTGACAGGCGCGGAGAGATAGGAG 495
 QY 241 TGCAGGAGTGTGAGAGCGGCTCTTACGCGTTTCAGAAACCAACCTCAGACCTGCTC 300
 Db 496 TGCAGGAGTGTGAGAGCGGCTCTTACGCGTTTCAGAAACCAACCTCAGACCTGCTC 555
 QY 301 AGCTGTCCAAATGCCAAGAAATGAGTGCAGGTGAGATCTTCTTCCAGAGTGGAC 360
 Db 556 AGCTGTCCAAATGCCAAGAAATGAGTGCAGGTGAGATCTTCTTCCAGAGTGGAC 615
 QY 361 CGGACACCGTGTGTGCTGCTGAGAGAACACGATACCGGCTTATTTGAGTGAACCTT 420

Db 616 CGGACACCGTGTGTGCTGCGAGAAACAGTACCGGCAATTATTTGGAGTGAACAACTT 675
Qy 421 TTCCAGTCTTCAATTGACAGCTCTGCTCAATGGGACCGTGCACCTTCTGCGCAGAG 480
Db 676 TTCCAGTCTTCAATTGACAGCTCTGCTCAATGGGACCGTGCACCTTCTGCGCAGAG 735
Qy 481 AAACGACACCGTGTGACCTGACAGTTTCTTTCTAAGAAAGAGAGTGTCTC 540
Db 736 AAACGAAACACCGTGTGACAGCTGACAGTTTCTTTCTAAGAAAGAGAGTGTCTC 795
Qy 541 TCCGTGTACTGTATGAGAAAAAGCTGAGTGCACAGAAATTGTGCTTACCCAGATGTAG 600
Db 796 TCCGTGTACTGTATGAGAAAAAGCTGAGTGCACAGAAATTGTGCTTACCCAGATGTAG 855
Qy 601 AATGTTAAGGGCAGTGAAGAGTCAAGGACACAGTGTGTGCTGCTGCTGCTTCTTT 660
Db 856 AATGTTAAGGGCAGTGAAGAGTCAAGGACACAGTGTGTGCTGCTGCTGCTTCTTT 915
Qy 661 GGTCTTTGCTTTTATCCCTCTCTTCAATGTTTATGTTATGCTTACCAAGGTTGAG 720
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Db 1156 CCCGCTGACTGTCCCACTTTTGGGCTCCCGCAGAGAGTGGACCAACCTATCAGGGG 1215
Qy 961 GCTGACCCCATCTTTGCGACAGCCCTGCGCTCCGACCCCATCCCAACCCCTTCAAG 1020
Db 1216 GCTGACCCCATCTTTGCGACAGCCCTGCGCTCCGACCCCATCCCAACCCCTTCAAG 1275
Qy 1021 TGGGAGAGAGGCGCCACAGGACAGAGCTAGACACTGATGACCCCGCGAGCTGTAC 1080
Db 1276 TGGGAGAGAGGCGCCACAGGACAGAGCTAGACACTGATGACCCCGCGAGCTGTAC 1335
Qy 1081 GCGCTGTGTGAGAAAGTGCCTGCTGCTGCTGGAAGAAATTCGTGCGCGCTTAGGGCTG 1140
Db 1336 GCGCTGTGTGAGAAAGTGCCTGCTGCTGCTGGAAGAAATTCGTGCGCGCTTAGGGCTG 1395
Qy 1141 AGCGACACAGAGATGATGCGCTGAGTGCAGAAAGGGGCGCTGCTGCGCGAGCGCNA 1200
Db 1396 AGCGACACAGAGATGATGCGCTGAGTGCAGAAAGGGGCGCTGCTGCGCGAGCGCNA 1455
Qy 1201 TACACAGATGCTGGGACACTGAGAGGGGGGACGCGCGCGCGGAGCCACAGCTGAGACTG 1260
Db 1456 TACACAGATGCTGGGACACTGAGAGGGGGGACGCGCGCGCGGAGCCACAGCTGAGACTG 1515
Qy 1261 CTGGAGACCGTGTCTCGGACATGAGACTGTGAGCTGCTGCTGAGAGATCGAGAGCGG 1320
Db 1516 CTGGAGACCGTGTCTCGGACATGAGACTGTGAGCTGCTGCTGAGAGATCGAGAGCGG 1575
Qy 1321 CTTTGGGCGCGCGCGCGCTCCGCGCGCGCGCGCGAGTCTTTCAGATGA 1368
Db 1576 CTTTGGGCGCGCGCGCGCTCCGCGCGCGCGCGCGAGTCTTTCAGATGA 1623

RESULT 5
US-08-126-016-1
; Sequence 1, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
; APPLICANT: WALLACH, DAVID

APPLICANT: NOPAR, YARON
APPLICANT: KEMPER, OLIVER
APPLICANT: ENGELMANN, HARTMUT
APPLICANT: BRAKEBUSH, CORD
APPLICANT: ADERKA, DAN
TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-1)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,016
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 319..1620
US-08-126-016-1
Query Match 99.9%; Score 1366.4; DB 1; Length 2175;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 301 AGCTGCTCAAAATGCCGAAAGAAATGGGTGAGTCTCTTCTTGCACAGTGGAC 360
D 556 AGTGTCTCAAAATGCCGAAAGAAATGGGTGAGTCTCTTCTTGCACAGTGGAC 615
QY 361 CGGACACCGGTGTGGTGTGAGAGAACAGTACCGGCAATTATTGGAGTGAAGACCTT 420
D 616 CGGACACCGGTGTGGTGTGAGAGAACAGTACCGGCAATTATTGGAGTGAAGACCTT 675
QY 421 TTCCAGTGTCTCAATGTGAGGCTGTGCTCAATGGGACCGGCACTCTCTGCGACGAG 480
D 676 TTCCAGTGTCTCAATGTGAGGCTGTGCTCAATGGGACCGGCACTCTCTGCGACGAG 735
QY 481 AAACAGAACACCGGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCT 540
D 736 AAACAGAACACCGGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCT 795
QY 541 TCCGTGTGTAATCTTAAGAAAAGCCCTGGAGTGCAGAAAGTGTGCTTACCCAGATTGAG 600
D 796 TCCGTGTGTAATCTTAAGAAAAGCCCTGGAGTGCAGAAAGTGTGCTTACCCAGATTGAG 855
QY 601 AATGTAAAGGCACTGAGGACTCAGGACCAAGTGTGCTTACCCAGATTGAG 660
D 856 AATGTAAAGGCACTGAGGACTCAGGACCAAGTGTGCTTACCCAGATTGAG 915
QY 661 GGTCTTGTGCTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
D 916 GGTCTTGTGCTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 975
QY 722 TCCAAAGTCTACCTCAATGTTTGTGGGAAATCCGACACCTGAAAAGAGGGGAGACTTGA 780
D 976 TCCAAAGTCTACCTCAATGTTTGTGGGAAATCCGACACCTGAAAAGAGGGGAGACTTGA 1035
QY 781 GGAATCTACTAAGCCCTGGCCCAACCAAGCTTCAAGTCTCAAGTCTCAAGTCTCAAG 840
D 1036 GGAATCTACTAAGCCCTGGCCCAACCAAGCTTCAAGTCTCAAGTCTCAAGTCTCAAG 1095
QY 841 CCCACCTGGGCTTCAAGTCTGGCCCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAG 900
D 1096 CCCACCTGGGCTTCAAGTCTGGCCCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAG 1155
QY 901 CCCGATGATCTGCTCAACTTGGGCGTCCCGGACAGAGAGTGGGACCAAGTCAAGGAG 960
D 1156 CCCGATGATCTGCTCAACTTGGGCGTCCCGGACAGAGAGTGGGACCAAGTCAAGGAG 1215
QY 961 GCTGACCCCAATCTTGGGACAGCCCTGGGCTCCGACCCCAAGTCTCAAGGAG 1020
D 1216 GCTGACCCCAATCTTGGGACAGCCCTGGGCTCCGACCCCAAGTCTCAAGGAG 1275
QY 1021 TGGGAGGACAGCGCCCAAGGACAGAGGCTTACAGTACAGTACAGTACAGTACAGT 1080
D 1276 TGGGAGGACAGCGCCCAAGGACAGAGGCTTACAGTACAGTACAGTACAGTACAGT 1335
QY 1081 GCGGTGTGAGAGAGTGGGCGTGGGCTGGGAGAGAAATTTGGGCGGCGCTTACGAGG 1140
D 1336 GCGGTGTGAGAGAGTGGGCGTGGGCTGGGAGAGAAATTTGGGCGGCGCTTACGAGG 1395
QY 1141 AGGACACAGAGATGATCGGCTGGAGCTCAGAAAGGCGGCTGCTGGCGAGAGCCAA 1200
D 1396 AGGACACAGAGATGATCGGCTGGAGCTCAGAAAGGCGGCTGCTGGCGAGAGCCAA 1455
QY 1201 TACAGCATGTGCGGACCTGAGAGCGGCGGACGCGCGGCGGCGGCGGCGGCGGCG 1260
D 1456 TACAGCATGTGCGGACCTGAGAGCGGCGGACGCGCGGCGGCGGCGGCGGCGGCGG 1515
QY 1261 CTGGGAGCGGTGCTCCGCGACATGAGCTCTGGGCTGCTGGAGGACATGAGAGGCG 1320
D 1516 CTGGGAGCGGTGCTCCGCGACATGAGCTCTGGGCTGCTGGAGGACATGAGAGGCG 1575
QY 1321 CTTTGGGCGCGCGGCGCTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1368
D 1576 CTTTGGGCGCGCGGCGCTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1623
```

```
RESULT 6
US-08-054-970-1
; Sequence 1, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054, 970
; FILING DATE: 03-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1620
; US-08-054-970-1

Query Match 99.9%; Score 1366.4; DB 4; Length 2175;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTCTTCACACCGTGCAGCTGTGCTGCACACTGGTGTCTGAGAGTGTGGTG 60
D 256 ATGGGCTCTTCACACCGTGCAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 315
QY 61 GGAATATATCCCTTCAGGGGTTATTGAGTGTGCTGCTTACCTAAGGGGACAGGAGAGAGA 120
D 316 GGAATATATCCCTTCAGGGGTTATTGAGTGTGCTGCTTACCTAAGGGGACAGGAGAGAGA 375
QY 121 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAATAATATGATTGCTGTAC 180
D 376 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAATAATATGATTGCTGTAC 435
QY 181 AAGTGCCAAAGAAAGAACTTGTACATGACTGTCCAGGCGCGGCGGCGAGATAGAGAC 240
D 436 AAGTGCCAAAGAAAGAACTTGTACATGACTGTCCAGGCGCGGCGGCGAGATAGAGAC 495
QY 241 TGCAGGAGGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAAACACCTCAGACACTGCTC 300
D 496 TGCAGGAGGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAAACACCTCAGACACTGCTC 555
QY 301 AGCTGTCTCAAAATGCCGAAAGAAATGGGTGAGTCTCTTCTTGCACAGTGGAC 360
D 556 AGCTGTCTCAAAATGCCGAAAGAAATGGGTGAGTCTCTTCTTGCACAGTGGAC 615
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Qy 361 CGGACACCGTGTGTGCTGCAGAGAAACAGTACCGGCAATTAATGAGTGAACCTT 420
Db 616 CGGGACACCGTGTGTGCTGCAGAGAAACAGTACCGGCAATTAATGAGTGAACCTT 675
Qy 421 TTCCAGTGTCTCAATGAGAGCTTGCCTCAATGGGACCGTGCACCTTCTCTCCAGAG 480
Db 676 TTCCAGTGTCTCAATGAGAGCTTGCCTCAATGGGACCGTGCACCTTCTCTCCAGAG 735
Qy 481 AAACAGAACACCGTGTGTGCTGCAGAGAAACAGTACCGGCAATTAATGAGTGAACCTT 540
Db 736 AAACAGAACACCGTGTGTGCTGCAGAGAAACAGTACCGGCAATTAATGAGTGAACCTT 795
Qy 541 TCCTGTAGTACTGTAAAGAAAAGCTGGAGTGCAGAGAAATGTGCTGCCAGATTGAG 600
Db 796 TCCTGTAGTACTGTAAAGAAAAGCTGGAGTGCAGAGAAATGTGCTGCCAGATTGAG 855
Qy 601 AATGTTAAGGACAGTGCAGAGTGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 856 AATGTTAAGGACAGTGCAGAGTGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 915
Qy 661 GGTCTTTCCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 916 GGTCTTTCCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 975
Qy 721 TCACAGCTCTACTGCTCATTTGTTGTGGAAATCGACACCTGAAAGAGAGGAGCTTGA 780
Db 976 TCACAGCTCTACTGCTCATTTGTTGTGGAAATCGACACCTGAAAGAGAGGAGCTTGA 1035
Qy 781 GGAATCTACTAAGCCCCCTGGCCCAACCAAGCTTCACTGCCACTTCAGAGCTTCAAC 840
Db 1036 GGAATCTACTAAGCCCCCTGGCCCAACCAAGCTTCACTGCCACTTCAGAGCTTCAAC 1095
Qy 841 CCCACCTCTGGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 1096 CCCACCTCTGGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1155
Qy 901 CCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 1156 CCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1215
Qy 961 GCTGACCCCATCTCTGTCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
Db 1216 GCTGACCCCATCTCTGTCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1275
Qy 1021 TGGAGAGACAGCGCCACAGCCAGAGCTAGACACTGATGACCCCGCAGAGCTGTAC 1080
Db 1276 TGGAGAGACAGCGCCACAGCCAGAGCTAGACACTGATGACCCCGCAGAGCTGTAC 1335
Qy 1081 GCGGTGTGTGAGAAACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1336 GCGGTGTGTGAGAAACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1395
Qy 1141 AGCGACACAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 1396 AGCGACACAGAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1455
Qy 1201 TACAGCATGTGTGCGAGCTTGAAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCTG 1260
Db 1456 TACAGCATGTGTGCGAGCTTGAAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCTG 1515
Qy 1261 CTGGAGAGCGTGTGCGAGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1516 CTGGAGAGCGTGTGCGAGAGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1575
Qy 1321 CTTTTCGCTG 1368
Db 1576 CTTTTCGCTG 1623

RESULT 7
US-08-050-319B-24
; Sequence 24, Application US/08050319B

Patent No. 5633145
: GENERAL INFORMATION:
: APPLICANT: M. Feldmann, P. W. Gray,
: APPLICANT: M. J. C. Turner, F. M. Brennan
: TITLE OF INVENTION: Modified human TNFalpha (Tumor
: TITLE OF INVENTION: Necrosis Factor alpha) Receptor
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Reed & Robblins
: STREET: 635 Bryant Street
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent in Release #1.0, version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/050,319B
: FILING DATE: 10-May-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Robbins, Roberta L.
: REGISTRATION NUMBER: 33,208
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 617-8999
: TELEFAX: (415) 327-3231
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2062 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 155..1519
: US-08-050-319B-24
Query Match 99.4%; Score 1360; DB 1; Length 2062;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1363; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ATGGGCTCTCTCCACCGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 155 ATGGGCTCTCTCCACCGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214
Qy 61 GGAATATACCCCTCAGGGGTTATTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 215 GGAATATACCCCTCAGGGGTTATTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 274
Qy 121 GATAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 275 GATAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 334
Qy 181 AAGTGCCCAAGAAAGAACTTGTACAAATGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 335 AAGTGCCCAAGAAAGAACTTGTACAAATGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 394
Qy 241 TGCAGAGAGTGTGAGAGGGGCTCTCTACCGCGCTTCAAGAAACACACTGACACTGCTGCTGCT 300
Db 395 TGCAGAGAGTGTGAGAGGGGCTCTCTACCGCGCTTCAAGAAACACACTGACACTGCTGCTGCT 454
Qy 301 AGCTGCTCCAATGCGCGGAAAGAAATGCGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 455 AGCTGCTCCAATGCGCGGAAAGAAATGCGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
Qy 361 CGGACACCGTGTGTGCTGCAGAGAAACAGTACCGGCAATTAATGAGTGAACCTT 420
Db 515 CGGACACCGTGTGTGCTGCAGAGAAACAGTACCGGCAATTAATGAGTGAACCTT 574

421 TTCAGAGCTTCATTAATTCAGAGCTTCGCTCAATGGAGACCTGACCTCTCTGCCAGAG 480
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575 TTCAGAGCTTCATTAATTCAGAGCTTCGCTCAATGGAGACCTGACCTCTCTGCCAGAG 634
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481 AAACAGAACACCGGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 540
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635 AAACAGAACACCGGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 694
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541 TCCTGTAGTACTGTAAAGAAAAGCTGGAGTGCAGAGATGTGCTGCTACCCAGATTGAG 600
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695 TCCTGTAGTACTGTAAAGAAAAGCTGGAGTGCAGAGATGTGCTGCTACCCAGATTGAG 754
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601 AATGTTAAGGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 660
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755 AATGTTAAGGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 814
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661 GGTCTTTGGCTTTTATCCCT 720
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815 GGTCTTTGGCTTTTATCCCT 874
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721 TCCAGAGCTTCATTAATTCAGAGCTTCGCTCAATGGAGACCTGACCTCTCTGCCAGAG 780
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875 TCCAGAGCTTCATTAATTCAGAGCTTCGCTCAATGGAGACCTGACCTCTCTGCCAGAG 934
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781 GGAAGTACTACTAAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 840
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935 GGAAGTACTACTAAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 994
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841 CCCAGCTTCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 900
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995 CCCAGCTTCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1054
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901 CCCAGCTTCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 960
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1055 CCCAGCTTCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1114
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961 GGTGAGAGCTTCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1020
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1115 GGTGAGAGCTTCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1174
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1021 TGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
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1175 TGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1234
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1081 GCGGTGTGTGAGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1140
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1235 GCGGTGTGTGAGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1294
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1141 AGCGAGACAGAGATGAGTGGGTGAGAGTGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
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1295 AGCGAGACAGAGATGAGTGGGTGAGAGTGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1354
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1201 TACAGAGATGCTGGAGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
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1355 TACAGAGATGCTGGAGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1414
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1261 CTGGAGAGGAGTGTCTCCGAGACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
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1415 CTGGAGAGGAGTGTCTCCGAGACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1474
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1321 CTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1368
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1475 CTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1522
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RESULT 9
US-08-762-308-10
: Sequence 10, Application US/08762308
: Patent No. 5925548
: GENERAL INFORMATION:
: APPLICANT: Beutler, Bruce A.
: APPLICANT: Bazoni, Flavia M.
: TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY

TITLE OF INVENTION: SIGNAL
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/762.308
FILING DATE: 09-DEC-1996
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: USSD:335--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 418-3000
TELEFAX: 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-762-308-10

Query Match 50.5% Score 690.4 DB 2 Length 1956:
Best Local Similarity 72.2% Pred No. 3.3e-156:
Matches 975: Conservative 0: Mismatches 351: Indels 24: Gaps 5:
QY 1 ATGGGCTCTCCACGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
DB 96 ATGGGCTCTCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 155
QY 61 GGAATATACCCCTCAGAGGCTTATTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 156 GGGATATACCTCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 215
QY 121 GATAGTGTGTGCCAAGGAAATATATCCACCTGCAAAATTAATTGATTTGCTGTACC 180
DB 216 GATAGTGTGTGCCAAGGAAATATATCCACCTGCAAAATTAATTGATTTGCTGTACC 275
QY 181 AAGTGCACAAAGAAACCTACTTGTACATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 276 AAGTGCACAAAGAAACCTACTTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 335
QY 241 TGCAGAGAGTGTGAGAGGAGGCTGCTTACACCGCTTCAAGAAACACCTGACAGACAGCTGCTG 300
DB 336 TGCAGAGAGTGTGAGAAAGGAGGACCTTACGCTTCCAGAAATTAATTGCTGAGGAGTGTCTG 395
QY 301 ACCTGCTCCAAATGTGCGAAAGAAATGAGGTGAGGTGAGATGCTCTTCTGACAGTGTGAC 360
DB 396 AGTTGCAAGACATGTGCGAAAGAAATGCTCCAGGTGTGAGATCTTCTGCTGCTGCTGCTGCTG 455
QY 361 CGGAGACCGCTGTGCTGCTGAGAGAAACGATACCGGATATTGAGTGAACCTT 420
DB 456 AAGGACACGCTGTGCTGCTGTAAGGAGAACGATTTCAACGCTTACTGAGTGTGAGACAC 515
QY 421 TTCAGAGTGTTAATTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 516 TTCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 575
QY 481 AAACAGAACACCGGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 540

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: palin (Genentech)
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/286,740
;; FILING DATE: 05-AUG-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER:
;; REFERENCE/DOCKET NUMBER: 798
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-1994
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;;
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6889 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;;
US-08-286-740-2

Query Match 46.2%; Score 632.4; DB 1; Length 6889;
Best Local Similarity 99.8%; Pred. No. 3,7e-142;
Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCGCTCCACCGTGCACCTGCTGTCACCTGTCCTCCAGACCTGTCGAGACCTTTGGTG 60
DB 1605 ATGGGCGCTCCACCGTGCACCTGCTGTCGCGGTGCTGCTGAGACCTTTGGTG 1664
QY 61 GGAATATACCCCTCAGGGGTTATTGACTGTCCTCACCAGAGGGGACAGGAGAGA 120
DB 1665 GGAATATACCCCTCAGGGGTTATTGACTGTCCTCACCAGAGGGGACAGGAGAGA 1724
QY 121 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCTCAAAATTAATTCGATTGCTGTACC 180
DB 1725 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCTCAAAATTAATTCGATTGCTGTACC 1784
QY 181 AAGTGCCCAAAAGGAAGCACTTGTACAAATGACTGTCCAGGCCCGGGGACAGATACGGAC 240
DB 1785 AAGTGCCCAAAAGGAAGCACTTGTACAAATGACTGTCCAGGCCCGGGGACAGATACGGAC 1844
QY 241 TGCAGGAGTGTGAGACGGGCTCTTCACCGCTTCAGAAAAACACCTCAGACACTGCTC 300
DB 1845 TGCAGGAGTGTGAGACGGGCTCTTCACCGCTTCAGAAAAACACCTCAGACACTGCTC 1904
QY 301 AGCTGTCCCAATGCCGAAAGGAATGGGTGAGGTGAGATCTTCTTTCGACAGTGGAC 360
DB 1905 AGCTGTCCCAATGCCGAAAGGAATGGGTGAGGTGAGATCTTCTTTCGACAGTGGAC 1964
QY 361 CGGAGACACCGTGTGGCTGAGAGAAACAGTACCGGCAATTTTGGAGTGAAGAACTT 420
DB 1965 CGGAGACACCGTGTGGCTGAGAGAAACAGTACCGGCAATTTTGGAGTGAAGAACTT 2024
QY 421 TTCAGAGCTTCAATTCAGAGCTGTGCCTCAATGGAGCGGTGACCTCTCTGCGCAGAG 480
DB 2025 TTCAGAGCTTCAATTCAGAGCTGTGCCTCAATGGAGCGGTGACCTCTCTGCGCAGAG 2084
QY 481 AAACAGAAACCGTGTGACACTGACATGAGGTTCTTTCTAAGAGAAAAGAGTGTGC 540
DB 1785 AAACAGAAACCGTGTGACACTGACATGAGGTTCTTTCTAAGAGAAAAGAGTGTGC 540

DB 2085 AAACAGAAACCGTGTGACACTGACATGAGGTTCTTTCTAAGAGAAAAGAGTGTGC 2144
QY 541 TCCTGTAGTACTGTAAAGAAAGCCTGGAGTGCAGGAAGTTGTGCTACCCAGATTGAG 600
DB 2145 TCCTGTAGTACTGTAAAGAAAGCCTGGAGTGCAGGAAGTTGTGCTACCCAGATTGAG 2204
QY 601 AATGTTAAGGCACTGAGACTGAGGACGACACAG 634
DB 2205 AATGTTAAGGCACTGAGACTGAGGACGACACAG 2238

RESULT 13
PCT-US95-09576-2
Sequence 2, Application PC/TUS9509576
GENERAL INFORMATION:

;; APPLICANT: GENENTECH, INC.
;; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
;; TITLE OF INVENTION: HOST CELLS
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: palin (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/09576
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/286740
;; FILING DATE: 05-AUG-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 00,000
;; REFERENCE/DOCKET NUMBER: 798PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-1994
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;;
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6889 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;;
PCT-US95-09576-2

Query Match 46.2%; Score 632.4; DB 5; Length 6889;
Best Local Similarity 99.8%; Pred. No. 3,7e-142;
Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCGCTCCACCGTGCACCTGCTGTCACCTGTCCTCCAGACCTGTCGAGACCTTTGGTG 60
DB 1605 ATGGGCGCTCCACCGTGCACCTGCTGTCGCGGTGCTGCTGAGACCTTTGGTG 1664
QY 61 GGAATATACCCCTCAGGGGTTATTGACTGTCCTCACCAGAGGGGACAGGAGAGA 120
DB 1665 GGAATATACCCCTCAGGGGTTATTGACTGTCCTCACCAGAGGGGACAGGAGAGA 1724
QY 121 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCTCAAAATTAATTCGATTGCTGTACC 180
DB 1725 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCTCAAAATTAATTCGATTGCTGTACC 1784
QY 181 AAGTGCCCAAAAGGAAGCACTTGTACAAATGACTGTCCAGGCCCGGGGACAGATACGGAC 240
DB 1785 AAGTGCCCAAAAGGAAGCACTTGTACAAATGACTGTCCAGGCCCGGGGACAGATACGGAC 1844

